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Perfect score:
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Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  post-processing:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 1s derived by analysis of the total score distribution.
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1 EVQLLESGGGLVQPG
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length: 2000000000
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Gapop 10.0 ,
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Copyright (c) 1993 - 2003 Compugen Ltd
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Maximum Match 1008
Listing first 45 summaries
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    888.
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                   y heavy chain v r
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g heavy chain - h
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: 22-Nov-1933 #sequence_revision 10-Nov-195
C; Date: 22-Nov-1933 #sequence_revision 10-Nov-195
C; Accession: $31686
R; Cuisinier A.M.; Gauthier, L.; Boubli, L.; Foug
R; Cuisinier A.M.; Gauthier S31686
A; Reference number: S31585
A; Reference number: S31585
A; Recession: S31686
A; Cetario: Tariosari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Hesidues: 1-140 <CUI>
A; Hesidues: 1-140 <CUI>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin C; Keywords: heterotetramer; immunoglobulin C; Keywords: heterotetramer; immunoglobulin
                               Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: How-1993 *sequence_revision 10-Nov-1995 *text_change 23-Jul-1999
C;C;Date: 22-Nov-1993 *sequence_revision 10-Nov-1995 *text_change 23-Jul-1999
C;Accession: S31588
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
C;Accession: S31588
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
C;Accession: S31588
A;Reference number: S31588
A;Accession: S31588
A;Accession: S31588
A;Accession: S31588
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A;Accession: S31588
A;Accession: S1588
A;Accession: S1588
A;Accession: S1588
A;Accession: S1588
A;Accession: S1640 <CUID
A;Cross -references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
A;Cross -references: EMBL:Z14200; NID:g30957; Immunoglobulin homology
C;Superfamily: immunoglobulin v region; immunoglobulin homology
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109; Conserv
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$31117
$46390
$31105
$31675
$31675
$26889
$46391
$31595
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5.7e-43;
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Length 140; Indels

5

Tonnelle, C.

C:Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Matches

Local

Similarity

90.98;

DB 2;

Length 140;

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C;Superfamily: in C;Keywords: hete. F;15-98/Domain:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                  Ig heavy chain
C;Species: Homo
C;Date: 02-Dec-
C;Accession: S3
                                                                                          A; Molecule type: mRNA
A; Residues: 1-123 < RAA>
                                                                        A; Cross-references: EMBL: X62963
                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                               K: Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A; Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                  C;Accession: S31114
R;Raaphorst, F.M.; T
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October C;Keywords: heterotetramer; immunoglobulin homology
                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 02-Dec:193  #sequence_revision 26-May-1995  #text_change 17-Mar-1999
C;Accession: S31107
C;Accession: S31107
Expression: S31107
Figure 1. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Accession: S31107
A;Accession: S31107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-119 < RAA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary; nucleic acid sequence not shown; translation not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKP-----FPYFDYWGQGTLVTVS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.7%;
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   Pred. No. 1.6e
5; Mismatches
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Pred. No. 1.5e-42;
6; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                  1.6e-42;
2;
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A;Cross-references: EMBL:X62956
A;Note: the nucleotide sequence was submitted to the EN
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMN>
                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 02-Dec-1903 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31108
R;Raaphorst, F.M., Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp A;Accession: S31108
A;Accession: S31108
                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
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C;Superfamily: immunoglobulin V region; immunc
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable
A:Reference number: A36005; MUID:90349571; PMID:2117273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-119 <SCH>
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Best Local Similarity
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These 108; Conservative
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         al Similarity 89 (
                                                                                                                                                                                                                                                                                                                                       107;
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                  89.7%;
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Score 545.5;
Pred. No. 5.5e
4; Mismatches
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Pred. No. 2.4e-42;
5; Mismatches 4; Indels 3
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; Pred. No. 1.6e-42; 
4; Mismatches 4;
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            .5e-42;
                            DB
                                                                  EMBL Data Library, October 1991
in homology
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                    Length 119;
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Indels

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Gaps

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RESULT 7

$31666

Ig heavy chain V region - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: $31666
R; Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate in A; Reference number: $31585
A; Reference number: $31585
A; Recession: $31666
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-138 <CUI>
A; Residues: 1-138 <CUI>
A; Cross-references: EMBL: 214202; NID: 930963; PIDN: CAA78571.1; PID: 930964
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology
F; 34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                      A;Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:g1340167 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-120 <MAH>
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ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRGFWSGYKDYWGQGTLVTVSS
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Pred. No. 6.4e-42;
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                                                                                                                                         Score 545; DB 2;
Pred. No. 6.1e-42;
4; Mismatches 5
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Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #te
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #te
C;Accession: S20782
R;Mortari, F.; Wang, J.; Schroeder, H.W.
R;Mortari, F.; Wang, J.; Schroeder, April 1992
R;Mortari, F.; Wang, J.; Schroeder, April 1992
R;Reference number: S20765
A;Recession: S20765
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-124 <MOR>
A;Residues: 1-124 <MOR>
A;Cross-references: EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:g33898
A;Cross-references: EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:g33898
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;15-98/Domain: immunoglobulin homology <IMM>
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D36005
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R;Schroeder Jr., H.W.; Wang, J.Y.

R;Schroeder Jr., H.W.; Wang, Jr., H.W.; Wang, Jr.Y.

R;Schroeder Jr., H.W.; Wang, Jr., H.
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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990
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A;Cross-references: GDB:118731; OMIM:146910
A;App position: 14q32.33-14q32.33
C;Superfamily; immunoglobulin V region; immunoc;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-119 <SCH>
A; Cross-references: GB:M34024
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Pred. No. 7.8e-42;
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                                                                                                                                                                                                                                                                                                 Score 538.5; DB Pred. No. 2.3e-41
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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995,#text_change 23-Jul-1999
C;Accession: S38489
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A; Residues: 1-127 <MAR>
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C: Superfamily: immunoglobulin V region;
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A; Residues: 1-121 <RES>
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Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
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Exp. Med. 178, 1903-1911, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
          QGTLVTV 127
                                                                          QGTLVTV 114
                                                                                                                        ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKEGPFPASDYYDSSGYYSFDYWG
                                                                                                                                                                      ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK--PFP-----YFDYWG
                                                                                                                                                                                                                                                            QVQLVQSGGGVVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
                                                                                                                                                                                                                                                                                                      EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVQLLESGGGLVQPGGSLRLSCTASGFTFSTYGMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 535.5; DB 2
Pred. No. 4.6e-41;
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Pred. No. 4.4e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X14584
C;Superfamily: immunoglobulin V region; im
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-144 <KIS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains
A;Reference number: S04601; MUID:89296497; PMID:2500644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate A;Reference number: S31585

A;Accession: S31699

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <CUI>
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A;Connection of the county of t
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A; Cross-references: EMBL: X14584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change C;Accession: S05271; S04602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:z14201; NID:g30961; PIDN:CAA78570.1; PID:g30962 C;Superfamily: immunoglobulin v region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin c;34-117/Domain: immunoglobulin homology <IMM>
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C:Accession: C:A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: S05270 A;Accession: S05271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, March 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Kishimoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain precursor - human (fragment)
C; Species: Homo sapiens (man)
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Best Local :
                                                                                                                                                                                                                                                                                            Matches 104;
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                                       ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK------PFPYF--DYWGQGTL 111
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   ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAVVRGVISYYYYGMDVWGQGTT
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Pred. No. 3.7e-40;
7; Mismatches 5;
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submitted to the EMBL Data Library, October 1992
A; Reference number: S30520
A; Reference number: S30520
A; Recession: S30531
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-125 <MARD
A; Cross references: EMBL: Z18317
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30531
R;Mariette, X.
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Search completed: August 20, 2003, 12:42:13 Job time : 82.0602 secs
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140 VTVSS 144
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US-08-983-607-28
                                                                                                              CLASSIFICATION: PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/IB96/01032
APPLICATION UNMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MATY M. KRINSKY
REGISTRATION UNMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
REGISTRATION INFORMATION:
TELEPHONE: 203-773-9544
TELEPHONE: 203-773-1183
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
TENGTH: 131 residues
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GENERAL INFORMATION:
APPITONIM
                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                              LENGTH: 131 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb
 ORIGINAL SOURCE:
ORGANISM: Homo sapi
ORGANISM: nized wit
INDIVIDUAL ISOLATE:
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CITY: New Haven
STATE: Connection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States of America
  Homo sapiens (melanoma patient immu-
nized with autologous tumor cells)
ISOLATE: peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Molecular Biophysics and Biochemistry, Yale University
                                                     polypeptide
                                                                                                                                                                                                                                                                                                                                   US/08/983,607
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US-08-983-607-46
US-08-428-197-26
US-08-428-197-28
US-08-428-197-28
PCT-US93-10555-24
PCT-US93-10555-28
US-08-428-197-2
PCT-US93-10555-28
US-08-983-607-51
PCT-US93-10555-2
US-08-983-607-51
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1,

2: /cgn2\_6/ptodata/1,

3: /cgn2\_6/ptodata/1,

4: /cgn2\_6/ptodata/1,

5: /cgn2\_6/ptodata/1,

6: /cgn2\_6/ptodata/1,

/cgn2\_6/ptodata/1/laa/5A\_COMB.pep:\*
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/cgn2\_6/ptodata/1/laa/6B\_COMB.pep:\*
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US-09-025-7698-38
US-09-025-7698-63
US-09-025-7698-178
US-08-974-899-6
US-08-98-1055-1
US-08-98-925-11
US-08-98-925-11
US-08-98-925-13
US-09-069-821-3
US-09-069-821-3
US-09-069-821-3
US-09-362-780-11
US-08-362-780-11
US-08-362-780-12
US-08-146-206C-21
US-08-146-206C-21
US-08-146-206C-21
US-08-1476-206C-21
US-08-1476-206C-20
US-08-1476-206C-20
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US-08-1476-206C-20
US-08-1476-206C-20
US-08-476-349A-99
US-08-476-349A-99
US-08-478-039-99
US-08-488-197-22
US-08-98-3-057-32
US-08-98-3-057-32
US-08-98-3-057-32

Sequence Sequence Sequence Sequence Sequence Sequence

Minimum DB Maximum DB Total number

seq length: seq length:

2000000000

of hits satisfying chosen parameters:

328717

328717 seqs, 42310858 residues

Scoring table: Sequence: Title: Perfect score:

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                                                         Query Match
Best Local :
                                       Matches
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Best Local Similarity
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                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        NAME: James F. Haley, Jr., I
REGISTION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MOI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/025,769B FILING DATE: 18-FEB-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                                                                                                                                                                                                                                                                                     FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: DM414
LIBRARY: fUSE5
                                                    Local
                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS/
SOFTWARE: Patentin Palace
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                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: V13
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                                       105;
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                                                    Similarity
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EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                               120 amino acids
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1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09025769B
                                    Conservative
                                                                                                                                                                                                                         (212)596-9090
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Plueckthun, Andreas
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Ilag, Vic
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oney, Simon
                                                  88.7%;
87.5%;
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                                Score 539; DB 4; Length 120, Pred. No. 5.7e-47; Findels 5; Indels
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Pred. No. 2e-47;
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                               4;
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Knappik, Achim

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US-09-025-769B-178
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Sequence 178, Application Patent No. 6300064 GENERAL INFORMATION:
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US-09-025-769B-63
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Best Local Similarity 87.5
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)596-909 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: (18-AUG-1995)

ATTORNEY/AGENT INFORMATION:
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APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 18-FEE
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                                                                                                                                                                                                                                                                                                                                                                1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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                                                                                                                                                                                                                               ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGOGTLYTVSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 120 amino acids
amino acid
GY: linear
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1251 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212)596-9090
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87.5%;
                                                                  US/09025769B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 539; DB 4;
Pred. No. 5.7e-47;
6; Mismatches 5
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Americas
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; TOPOLOGY: 11; MOLECULE TYPE: US-09-025-7698-178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acid
                                                                                                                                                                                                                                                                   sequence 6, Application US/08974899 vatent No. 6037454 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 9. FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
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APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
                                                                                                                                                                    APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: JArdieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 18-FE
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
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                                                                                                  STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                     COUNTRY:
                                                                                                                                                              DDRESSEE:
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1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                           USA
                                                                                                                                                              Genentech, Inc.
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SILVERMAN TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acid
TYPE: Amino Acid
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                          ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION UNMBER: 34,842
REFERENCE/DOCKET NUMBER: FD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley
                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT,
FILING DATE: 29-OCT-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/0 FILING DATE: 11/27/96 TORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                           ZIP: 90067
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                                                                                                                                                                                                 FILING DATE:
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                 TELEPHONE:
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Amino Acid
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1880 Century Park East - Suite 500
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650/952-9881
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(619)
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                    (619) 455-5100
   455-5110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
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Pred. No. 7.5e-47;
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PCT-US93-10555-1
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                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5110
TELEFAX: (619) 455-5110
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NFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 18/2
FEATURF:
                  TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MMEDIATE SOURCE:
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                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/
FILING DATE: 29-OCT-1993
                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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California
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                                                                   amino acid
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1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                  linear
                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
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                                                                                    amino acids
                peptide
                                                 single,
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Pred. No. 8.4e-47;
6; Mismatches
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US-08-983-607-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 203-773-1183 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                 MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 116 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 203-773-9544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/9
FILLING DATE: April 27, 1998
                                        MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alan Garen
APPLICANT: Xiaohong C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                       ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: ZU3 , TELEPH
                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/IB
FILING DATE: June 28, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 266 Whi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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DM414 scFv antibodies obtained from
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                                                                                                                                                                                                                                                                                    linear
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1..125
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84.0%;
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LIBRARY: fUSE5 fusion phage construct CLONE: V474
FEATURE:

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US-07-988-925-11
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Best Local S
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                                              Query Match
Best Local Similarity
                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                              TELEFAX: 7038164100
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                       FILING DATE: 21-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206422.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA;
APPLICATION NUMBER: WO PCT/GB92/01933
FILING DATE: 21-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Waldmann, Herman TITLE OF INVENTION: antibody preparation NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                           SEQUENCE CHARACTERISTICS
LENGTH: 119 amino acto
                                                                                              MOLECULE TYPE: peptide -988-925-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
                                                                                                                               TOPOLOGY:
                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                106;
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Similarity 87.9%;
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                                                                                                                                                            amino acid
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EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
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lith Floor, 1100 No. 5585097th Glebe Road
                                                                                                                                                                          119 amino acids
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                                                                                                                                linear
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                                                                                                                                            single
                                              87.9%;
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Pred. No. 1.4e-46;
                                <u>ب</u>
                                Score 534.5; DB 1;
Pred. No. 1.6e-46;
2; Mismatches 8;
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RESULT 10
US-08-362-780-11
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-362-780-11
            RESULT 11
US-09-069-821-3
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Sequence 3,
                                                                                                                                                                                              Matches 106;
                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/862,543
FILING DATE: 23-JUNE-1992
APPLICATION NUMBER: GB 9021679:7
FILING DATE: 05-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB91/01726
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CTTY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                              Local Similarity 89.1 les 106; Conservative
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                                                                                               61 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKPEPY---FDYWGQGTLVTVSS 116
                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
Application US/09069821
                                                                        8th Floor, 1100 No.
                                                                                                                                                                                                                                                                                                                                119 amino acids
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                                                                                                                                                                                                                                                                                    ss: single
linear
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h Floor, 1100 No. 5968509th Glebe Road
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BER: 29009
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                                                                                                                                                                                                              87.98;
89.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/362,780
                                                                                                                                                                                               2
                                                                                                                                                                                              Score 534.5; DB 2;
Pred. No. 1.6e-46;
                                                                                                                                                                                                                            Length 119;
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RESULT 12
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                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-UN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: (FILING DATE: 23-JUN-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/044,449 FILING DATE: 30-APR-1997 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION I
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 30-AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/063,074 FILING DATE: 27-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: STERNE, KESSLER, STREET: 1100 NEW YORK AVE.,
                                                                                                107
                                                                                                                           190 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGRXGXSLSGXYYYYHYFDYW 249
                                                                                                                                                                                         130 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGKTDGGST
                                                                 250
                                                                                                                                                                                                                                                                105;
                                                                                                                                                        59 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKP-----FPYFDYW 106
                                                                                                                                                                                                          1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSS--GTT 58
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                                                                                    GQGTLVTVSS 116
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KIM, JUDITH U.
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                                                                GQGTLYTYSS 259
                                                                                                                                                                                                                                                                                                                                                                                                        263 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHITLOW, MARC
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                                                                                                                                                                                                                                                                                                                                           peptide
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                                                                                                                                                                                                                                                                           87.3%;
80.8%;
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                                                                                                                                                                                                                                                                            Score 531;
Pred. No.
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                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                         DB 4; Length 263; .9e-46;
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PRIOR APPLICATION NUMBER: 60/369,860
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILLING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILLING DATE: 2001-11-14
PRIOR PRIOR APPLICATION NUMBER: 60/331,310
PRIOR APPLICATION NUMBER: 60/331,310
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Patent No. 6538938
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SOFTWARE: Patentin V
SEQ ID NO 6
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                                                                                                                                                                                                                                                     FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
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CURRENT FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/10-
PRIOR FILING DATE: 1998-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Extract Mang, Maoliang
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. 633396el Method for Targeted Delivery of Nucleic Acids
TITLE OF INVENTION: No. 633396el Method for Targeted Delivery of Nucleic Acids
TITLE OF TREERINGE: 0977.2300001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: UNSURE
LOCATION: (232)
OTHER INFORMATION: May be any amino
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TYPE: PRT
ORGANISM: Artificial Sequence
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LOCATION: (234)
OTHER INFORMATION: May be
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                                       APPLICATION NUMBER: 60/327,364 FILING DATE: 2001-10-09
                                                                              APPLICATION NUMBER: 60/331,044
FILING DATE: 2001-11-07
                 APPLICATION NUMBER: 60/323,807
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                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10039785
DATE:
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80.8%;
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Pred. No. 9.7e-46;
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FILING DATE: 2001-08-02 APPLICATION NUMBER: 60/ FILING DATE: 2001-06-04

60/294,981

2001-08-02

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Best Local Similarity
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NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
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TYPE: PRT
ORGANISM: Artificial sequence
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ent No. 5821337
                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
ETITIC NATE: 14-TIN-1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
                                                                                   FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/934,373C FILING DATE: 21-Aug-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: South San
                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WinPatin
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                   650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Francisco
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83.3%;
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US-08-437-642B-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6054297
GENERAL INFORMATION:
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                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                         FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
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                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                         SEQUENCE CHARACTERISTICS
                                                                                                        TELEPHONE: 650/225-1994
                                                                                                                                                                           FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Paul J. Ca
APPLICANT: Leonard G.
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0:
FILING DATE: 09-May-1995
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/1 FILING DATE: 17-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                  TYPE:
                                                                                         TELEFAX:
                                                                                                                                   REGISTRATION NUMBER: 40, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                       TELEPHONE:
                 TOPOLOGY:
                                             LENGTH:
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5. 6054297
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                                Amino Acid
                                                                                                                                                                Lee, Wendy M.
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                                                                                          650/952-9881
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                 Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genentech, Inc
                                                                                                                                                                                                                                     IUMBER: PCT/US92/05126
15-JUN-1992
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7.3e-46;
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Query Match

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Matches 10	Matches 103; Conservative 6; Mismatches 7; Indels - 6; Gaps 1;
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Db 1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSYISGDGGSTYY 60
Qy 61	61 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLYTV 114
Db 61	61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGRYGYSLSGLYDYWGQGTLYTV 120
Qy 115	115 SS 116
Db 121	121 SS 122
Search completed: Augus Job time : 81.3614 secs	Search completed: August 20, 2003, 12:44:16 Job time : 81.3614 secs

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Title:
Perfect score:
Sequence:
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

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6 US-10-291-265-807
7 US-10-336-041A-12
7 US-10-336-041A-13
7 US-10-336-041A-13
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9 US-10-407-610-1610
9 US-10-447-243-3
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  Sequence 1, Appli
Sequence 332, App
Sequence 334, App
Sequence 804, App
Sequence 805, App
Sequence 807, App
Sequence 10, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 16, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 171, Appl
Sequence 1718, Appl
Sequence 2752, Appl
Sequence 2711, Appl
Sequence 27128, Appl
Sequence 1718, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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بر بر	atch bal	; NAME/KEY: SITE; LOCATION: (131).( ; OTHER INFORMATION: ; FEATURE: ; OTHER INFORMATION: ; OTHER INFORMATION: ; OTHER INFORMATION: US-10-336-041A-1	FEATURE:  NAME/KEY:  LOCATION:  OTHER INFO FEATURE:	SEQ ID NO 1 LENGTH: 23 TYPE: PRT ORGANISM: FEATURE: NAME/KEY: LOCATION:	APPLICANT:  TITLE OF IN  FILE REFERE  CURRENT APP  CURRENT FIL  PRIOR APPLII  PRIOR FILIN  PRIOR FILIN  PRIOR FILIN  NUMBER OF S.  SOFTWARE: P	RESULT 1 US-10-336-041A- ; Sequence 1, A ; GENERAL INFOR	28 48 29 48 31 48 32 47 35 47 47 36 47 47 46 5 5 46 5 46 6 5 6 6 6 6 6 6 6 6 6 6
; Conservat	100. imilarity 100.	EY: SITE ON: (131)(238) INFORMATION: VL E: EN: DESCRIPTION: Description INFORMATION: antibody fr 041A-1	INFORMATION: VA RE: CON: (117)(130) INFORMATION: Linker RE:	H: 238 PRT ISM: Artificial Sequence RE: REY: SITE ION: (1)(116)	APPLICANT: SCHETING AG TITLE OF INVENTION: New methods FILE REFERENCE: 27041P_WOAS CURRENT APPLICATION NUMBER: US/ CURRENT FILING DATE: 2003-01-0 PRIOR APPLICATION NUMBER: EP02 PRIOR FILING DATE: 2002-01-03  PRIOR APPLICATION NUMBER: US60/ PRIOR FILING DATE: 2002-02-25 NUMBER OF SEQ ID NOS: 13 SOFTWARE: PatentIn Ver. 2.1	AL -041A-1 e 1, Application US/10336041A INFORMATION:	65.8 561 7 65.8 561 624 6 65.8 1487 6 65.8 1487 6 65.8 1487 6 65.4 4 39 6 64.4 620 6 64.4 620 6 64.4 620 6 64.4 627 6 65.0 134 6
. <b>4</b> 0;	0%; Score 73; DB 0%; Pred. No. 0.03	of Artificial agment		ice	ds for diagnosis 15/10/336,041A -03 12 000 315.8 	ALIGNMENTS	US-09-820-843B-19 US-60-490-890-1788 US-10-374-780A-1466 US-10-292-798-1370 US-10-292-798-1370 US-10-292-798-1375-62 US-10-603-113-20916 US-10-603-113-20916 US-10-286-897-3056 US-10-286-898A-3955 US-10-374-780A-795 US-10-258-898A-5714 US-10-258-898A-5714
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RESULT 2
US-10-291-265-332
Sequence 332, Application US/10291265
GENERAL INFORMATION:

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APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al
APPLICANT: Tang et al
ITILE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-74
PRIOR FILING DATE: 2000-01-74
PRIOR FILING DATE: 2000-01-75
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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                                                            Sequence 804, Application GENERAL INFORMATION:
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SEQ ID NO 334
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 334, Application US/10291265 GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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NUMBER OF SEQ ID NOS: 944
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TYPE: PRT
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                                                                                                                                                                            141 GDGSSGGSGGASTG 154
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136 GDGSSGGSGGASTG 149
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Pred. No. 0.041;
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Pred. No. 0.041;
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US-10-291-265-806
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US-10-291-265-805
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LENGTH: 384
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PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-15
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Best Local
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APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al
APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
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PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
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CURRENT FILING DATE: 2000-01-25
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CURRENT APPLICATION NUMBER: US/
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Pred. No. 0.05;
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Pred. No. 0.05;
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US-10-291-265-806
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US-10-336-041A-10
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PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
                                                                    Sequence 10, Application US/10336041A
GENERAL INFORMATION:
APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis and treatment of tumours
FILE REFERENCE: 27041P_WOAS
CURRENT APPLICATION NUMBER: US/10/336,041A
CURRENT FILING DATE: 2003-01-03
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SOFTWARE: FRATSEQ for Windows Version 3.0

SEQ ID NO 807

LENGTH: 384
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CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
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equence 807, A
PRIOR APPLICATION NUMBER: EPO2 000 315.8 PRIOR FILING DATE: 2002-01-03 PRIOR APPLICATION NUMBER: US60/358702 PRIOR FILING DATE: 2002-02-25
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R FILING DATE: 2000-07-17
R APPLICATION NUMBER: 09/631,451
R FILING DATE: 2000-08-03
R APPLICATION NUMBER: 09/633,870
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Pred. No. 0.05;
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Pred. No. 0.
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; OTHER INFORMATION: Description of Artificial Sequence: recombinant; OTHER INFORMATION: antibody fragment US-10-336-041A-10
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US-10-336-041A-11
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PRIOR FILING DATE: 2002-02-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 240
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APPLICANT: Schering AG
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SEQ ID NO 11
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TITLE OF INVENTION: New methods for diagnosis and treatment of tumours
FILE REFERENCE: 27041P_WOAS
CURRENT APPLICATION NUMBER: US/10/336,041A
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: EPD2 000 315.8
PRIOR FILING DATE: 2002-01-03
PRIOR FILING DATE: 2002-01-03
PRIOR FILING DATE: 2002-01-03
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CURRENT APPLICATION NUMBER: US/10/336,041A
CURRENT FILING DATE: 2003-01-03
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TYPE: PRT
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NUMBER OF SEQ ID NOS: 13
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                ORGANISM: Artificial Sequence
FEATURE:
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es 12; Conservat
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                                                                                             PatentIn Ver.
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100.0%; Pred. No. 0.
tive 0; Mismatches
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US-10-336-041A-9
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US-10-336-041A-9
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; OTHER INFORMATION: antibody fragment
US-10-336-041A-13
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US-10-336-041A-13
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                     Query Match
Best Local Similarity
                                                                                                                                                       NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 9
LENGTH: 247
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Schering AG
APPLICANT: INVENTION: New methods for diagnosis and treatment of tumours
         Matches
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GENERAL INFORMATION:
APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis and treatment of tumours
FILE REFERENCE: 27041P_WOAS
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Best Local
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Matches
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                                                                                 OTHER INFORMATION: Description of Artificial Sequence: recombinant OTHER INFORMATION: antibody fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1 EQ.ID NO 13
                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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100.0%; Pr
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100.0%; Pred. No.
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Pred. No.
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0.61;
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0.61;
                                  Length 247;
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US-10-273-973-16
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                          TELEFAX: 619-554-6312 INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                FRAGMENT TYPE:
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barbas, Carlos
Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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23 GGGSGGGSGGSEG 36
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                                  1 GDGSSGGSGGASTG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/133,011
FILING DATE: 08-JUN-1994
APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: The Scripps Research Institute, Office of Patent Counsel
STREET: 10666 North Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                   TOPOLOGY: unknown
                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22-Jan-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fitting, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/273,973
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71.4%;
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                                                                      Mismatches
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                                                                                                       Length 211;
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RESULT 14
US-60-485-404-55
; Sequence 55, Application US/60485404
; GENERAL INFORMATION:

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SEQ ID NO 55
SEQ ID NO 55
LENGTH: 433
TYPE: PRT
ORANUEM: artificial
FEATURE: INFORMATION: M13 pIII coat protein for insertion into pUC18 vectors
US-60-485-404-55
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
LENGTH: 498
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-10-225-838B-21
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US-10-225-838B-21
Search completed: August 20, 2003, 12:45:11 Job time: 4.04819 secs
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                                                                                                                                      Query Match
Best Local Similarity 64.3
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Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Neuronz, Ltd.
APPLICANT: Neuronz Biosciences, Inc.
APPLICANT: Sieg, Frank
APPLICANT: Sieg, Frank
APPLICANT: Hughes, Paul
TITLE OF INVENTION: Neural Regeneration Peptides and Methods for Their Use In
TITLE OF INVENTION: Treatment of Brain Damage
FILE REFERENCE: NRNZ-1023US1
CURRENT APPLICATION NUMBER: US/10/225,838B
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: 60/314,952
PRIOR FILING DATE: 2001-08-24
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PRIOR FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 75
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PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/406,997
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
PRIOR FILING DATE: 2003-03-10
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CURRENT FILING DATE: 2003-07-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: Transferrin Fusion Protein Libraries ILE REFERENCE: 054710-5007-PR
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                                                                                  434 GDGGDGGAGGNGTG 447
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Pred. No. 17;
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Perfect score:
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Maximum DB seq
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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A_Geneseq_19Jun03:*
A_Geneseq_19Jun03:*
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  AAY53773
AAE08818
AAY53775
AAU14227
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                                                                                                                                                                                                                                                                                                  SUMMARIES
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Ç	יו ני	335	335	335	334	319	301	LOT.	301	301	293	293	293	219	219	211	211	211	211	211	60	60	60	49	49	49	36	36	36	36	36	ა 5	296	318	928	384
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	ARG97767	AAE13994	AAY53200	AAR79319	ABBULZEO	AAU81746	ABG9 / / 66	MAELOUGO	AAYSJI99	AAR/9318	AAY9//90	AAY97794	AAR75660	AAY97686	AAY97677	AAY98191	AAY95082	AAR54281	AAR50174	AAR62927	ABG97801	AAE14028	AAR65750	ABG97800	AAE14027	AAR65749	774	390	213	AAR93972	AAR79295	AAW17096	AAY14121 .	122	ABB92408	AAU14464
	Human Interleukin-	Myelopoletin (MPO)	Human incerteukin-	IL-3 containing in	odcret tall po	Region #1 or pacce	#1 Of TO	•	Chemically modifie	•	Tag non part t	<b>.</b> ⊢	IS PILL IUS	rrom cons	from cons	CTO SEC IN	SEQ	M13 phage coat pro	nchor		Human interieukin-	Chemically modifie	Linker sequence us	Human interleukin-	Chemically modifie	Linker sequence us	Human interleukin-	Chemically modifie	Peptide Linker use	Highly flexible (G	rich spac	-derived ile	Raly protein seque	acterium	Herbicidally activ	ļ,

## ALIGNMENTS

AAY53773 standard; Peptide; 14

A A

22-FEB-2000 AAY53773;

(first entry)

scFv; antibody; ED-B domain epitope; fibronectin; marker; angiogenesis; vascular proliferation; diabetic retinopathy; age-related macular degeneration; tumour; immunoscintigraphic detection; blood coagulation; blood vessel occlusion; ocular angiogenesis; angiogenesis-related pathology. Synthetic. Linker of an antibody with improved specificity for fibronectin WPI; 2000-039074/03 11-MAY-1998; 28-APR-1999; 11-MAY-1999; 18-NOV-1999. (EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH. WO9958570-A2 Tarli L, 98US-0075338. 99US-0300425. 99WO-EP03210 Viti F, Birchler M;

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RESULT 2
AAE08818
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Best Local S
Matches 14
    The invention relates to
                                Claim 10; Page 36; 73pp;
                                                            An antibody, with specific affinity for a characteristic epitope of the ED-B domain of fibronectin for the treatment of diseases characterized by vascular proliferation - \,
                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this epitope was improved by introducing a number of mutations in the complementarity determining region (CDR) residues located at the periphery of the binding site. The improved antibody is used for rapid targeting markers of angiogenesis, for detecting diseases characterized by vascular proliferation, such as diabetic retinopathy, age-related macular degeneration or tumours. The antibody localizes the respective tissue within 3 to 4 hours after injection. It is used in immunoscintigraphic detection of angiogenesis and for diagnosis and therapy of tumours and diseases characterized by vascular proliferation. Coagulation and blood vessel occlusion. These conjugates are used in the preparation of injectable compositions for the treatment of angiogenesis-related pathologies, especially caused by or associated
                                                                                                                                                      Neri D,
                                                                                                                                                                                                                                                                                                                                                             SGFV; single-chain variable antibody fragment; coagulant; ED-B domain; fibronectin; tunnor; cvascular proliferation; rheumatoid arthritis; angiogenesis; blood coagulation.
                                                                                                                                                                                                                                                                          30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic peptide linker for constructing ScFv L19
                                                                                                                                                                                   (EIDG-)
                                                                                                                                                                                                             24-FEB-2000; 2000US-0512082
                                                                                                                                                                                                                                         23-FEB-2001; 2001WO-EP02062
                                                                                                                                                                                                                                                                                                      WO200162800-A1
                                                                                                                                                                                                                                                                                                                                   Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE08818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE08818 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibronectin
antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e present sequence represents a linker component of a modified human fv antibody which has specific affinity for a characteristic epitope the ED-B domain of fibronectin. The affinity of the antibody for
                                                                                                                        2001-541701/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocular angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                              EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH
                                                                                                                                                    Tarli L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDGSSGGSGGASTG 14
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ilarity 100.0%;
Conservative (
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                                                                                                                                                 Viti F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59pp; English.
an antibody with specific affinity for
                                English.
                                                                                                                                                   Birchler M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
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Pred. No. 0.0049;
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                                                                                                                                                                                                                                                                                                                                                                                                      fragment; cancer; cytotoxic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                         ocular
                                                                                                                                                                                                                                                                                                                                                                     blood vessel occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody.
                                                                                                                                                                                                                                                                                                                                                                                   disorder; psoriasis;
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RESULT 3
AAY53775
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                                                   The present sequence represents a modified human scFv antibody which has specific affinity for a characteristic epitope of the ED-B domain of fibronectin. The affinity of the antibody for this epitope was improved by introducing a number of mutations in the complementarity determining region (CDR) residues located at the periphery of the binding site. The improved antibody is used for rapid targeting marker of angiogenesis, for detecting diseases characterized by vascular and the complementarity determined by vascular and the complementarity det
                                                                                                                                                                                                                                                                Claim 10; Page -;
                                                                                                                                                                                                                                                                                                                     Fibronectin ED-B domain epitope specific antibodies and conjugate antibodies - ``
                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Neri
                                                                                                                                                                                                                                                                                                                   antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1998;
28-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful in the detection and/or coagulation of blood vessels. An antibody with improved affinity to the ED-B domain is useful for diagnosis and therapy of tumours and diseases characterised by vascular proliferation, cancer, rheumatoid arthritis, neo-vasculature associated coular disorders and psoriasis. Treatment of angiogenesis related pathologies comprises the injection of conjugates comprising antibody and a molecule capable of inducing blood coagulation and blood vessel occlusion. The present sequence is a peptide linker used for constructing single-chain variable antibody fragment (scFV) L19 antibody related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          age-related macular degeneration; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scFv; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY53775 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ED-B domain epitope; fibronectin; marker;
                                                                                                                                                                                                                                                           59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              improved specificity for fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                         Viti F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      blood vessel occlusion;
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0.0049;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      retinopathy;
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proliferation, such as diabetic retinopathy, age-related macular degeneration or tumours. The antibody localizes the respective t

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis
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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human novel protein #96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2000; 2000US-0491404.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
        The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberran protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the
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antibacterial; antiallergic;
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                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
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nervous system disorders,
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                                                                                                                                                                                                                                                         Liu C,
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                                                                                                                                   Page 576-577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Antianaemic; osteopathic; antiinflammatory; tory; cytostatic; neuroprotective; vulnerary; nootropic; nt; antiarthritic; cerebroprotective; antifungal; antivil; antiallergic; dermatological; haemostatic; antiasthma; immunogen; antibody; gene therapy; neurological disord disease; inflammatory disorder; cancer; asthma; osteopor
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                                                                                                                                                                    useful for treating anti-inflammatory diseases, ers, and for regenerating bone and cartilage -
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17-JUL-2000;
03-AUG-2000;
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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
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                                                                                                                   Claim
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antibodies
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                                                                                                                                                                                                                                              2001-476164/51.
DB; AAH98760.
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                                                                                                                                                                polypeptide for treatment es and research use -
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                                                                                                           Page 1102-1103; 1275pp;
                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312
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; 2000US-0617746.
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; 2000US-0663870.
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A, Zhang
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J, W
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                              Chen
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                                                                                                                                                                                   diagnostics, raising
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AAU14461
ID AAU
     The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and cantibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as complements, and in antibody production. Complex markers, food supplements, and in antibody production. Complex markers, food supplements, and in antibody production. Complex markers, for identify compounds which bind to the complex markers. For polypeptides are used to identify compounds which bind to the complex markers, for sequencing, for chromosome or gene mapping, in the complex markers, for sequencing, for chromosome or gene mapping, in the compound of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to carget drugs to a tumour, in assays to determine duantitative components antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet attached the complex markers and to be completed to the invention may also be useful in treating platelet.
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                                                                                                                                                                                                                                                                                                                    Example 4; Page 824-825;
                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS22766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatclogical; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   urchin and tomato. These were derived from expressed sequence to from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence protein of the invention.
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Pred. No.
                                                                                                                                                                                                                                                                                                                    English.
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disorders,

regenerating

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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to
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DB; AAS22767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GDGSSGGSGGASTG 14
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                                                                                                                                                                                                                                                                                                                                                                                                       Page 825-826; 894pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treating anti-inflammatory diseases, d for regenerating bone and cartilage -
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Pred. No.
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proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and
                                                                                                     The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antialiergic; dermatological; haemostatic; antiastimatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                         Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                            Example 4; Page 826-827;
                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2000; 2000US-0491404
                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2001; 2001WO-US02623.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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DB; AAS22768.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regeneration;
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                                                                                                                                                                                                                                                                                                        Liu C,
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                                                                                                                                                        894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                  by the aberrant
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RESULT 10
AAU14464
ID AAU144
XX AU14
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                WPI;
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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-OCT-2001
                                                                                                                                                                                                                    Isolated polypeptides useful for t nervous system disorders, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-)
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                                                                                                                                                                                                                                                                                                                   2001-451939/48.
)B; AAS22769.
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                                                                                                                                                            4; Page 827; 894pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein #335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; Antianaemic; osteopathic; antiinflammatory;
tory; cytostatic; neuroprotective; vulnerary; nootropic;
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Pred. No.
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                                                                                                                                                                                                                                                           treating
                                                                                                                                                                                                                    treating anti-inflammatory diseases, regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.14;
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RESULT 11
ABB92408
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein expression or activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB92408 standard;
                                                                                                                                  Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                    07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                         Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herbicidally active polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB92408;
                                                                                                                    organisms
                                                                                                                                                                                                                           Tietjen K, Weidler
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                                                                                                                                                                                                                                                                                                                     28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                          (FARB )
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                                                                                                                                                                                                2002-269010/31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The polypeptides can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 384;
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                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                          sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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(ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant nucleic acid or amino acid sequences from non-plant organisms suitable search parameters, where plant sequences having an E-value

E-value

plant

using

The invention relates (ABB90790-ABB94016) for

s to

identifying

target proteins

Claim 5;

SEQ .ID

NO 1619; 261pp + Sequence Listing;

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RESULT 12
ABB81229
ID ABB81
XX ABB81229
XX ABB81229
XX Mycob
XX I6-AI
XX I6
                                                                                                                                                                CC of interest invention describes a method for isolating a polynucleotide CC of interest that is present or is expressed in a genome of a first CC second mycobacterium strain and that is absent or altered in a genome of a CC using a bacterial artificial chromosome (BAC) vector. Recombinant BAC concerts, which are preferably immobilised, can be used to detect CC mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in bhological CC mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in bhological CC samples. The polynucleotides identified are useful as probes or primers CC polynucleotides contained in the recombinant BAC vectors it is possible to ophysically map a polynucleotide of mycobacterium of interest. By aligning the CC biological sample. The methods and vectors from the present invention possible to compare genomes between different strains or species and their non-pathogenic strains or species counterparts. ABG62422 to ABG6328 and ABB61227 to ABB61230 represent sequences used in the present invention can be compared the present invention contains of the present invention contains and ABB61227 to ABB61230 represent sequences used in the present invention can be compared the present invention can be compared to a bacterial counterparts. ABG62421 to ABG6328 and ABB61227 to ABB61230 represent sequences used in the present invention.
            Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       몽
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Best Local S
Matches 11
                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 6; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolation of polynucleotides from mycobacterial genomes, useful for detection of Mycobacteria and for combating tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-013262/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB81229 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buchrieser-Brosch R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                 318
                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ium tuberculosis; Mycobacterium bovis; mycobacterium;
BAC vector; bacterial artificial chromosome; tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis strain H37Rv PE-PGRS protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0060756
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                                     74.08;
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      Score 54; DB Pred. No. 27; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gordon S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Billault A;
                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
      2
                                                          Length 318
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      Indels
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Gaps
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Query Match 72.1 Best Local Similarity 71.. Matches 10; Conservative

72.6%;

; Score 53; DB; Pred. No. 33; 1; Mismatches

20; ω

Length 296; Indels

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Gaps

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RESULT 13
ANT14121
ANT ANT14
XX ANT14
XX ANT14
XX ANT14
XX PCR P
XX PCR P
XX PCR P
XX PCR P
XX YEAR
OS Synth
XX W0992
XX J-OC

                                                         This sequence is the Raly (RNP associated with lethal yellow) protein, CC DNA encoding it can be used in a specific engineered fragment (SEF). CC The invention relates to gene targeting vectors that comprise 2 yeast comparise invention relates to gene targeting vectors that comprise 2 yeast cC selectable marker, a mammalian cell selectable marker and gene-specific CC prepared by a method, comprising: (a) preparing a shuttle vector CC marker, and a fragment of genomic DNA containing at least part of a gene CC marker cassette comprising a SEF comprising a marker capable of CC marker cassette comprising a second yeast selectable marker different CC expression in mammalian embryonic stem cells and the marker cassette CC planked on each side by mammalian gene-specific flanking sequences CC yeast cells with a shuttle vector as in (a) and with a SEF as in (b), and CC ellowing the shuttle vector and the SEF to recombination; (d) selecting the transformed yeast cells for expression targeting vector yeast cells selectable marker; and (e) isolating the SEF from the yeast cells selectable marker; and (e) isolating the SEF from the yeast cells selectable marker; and (e) isolating the condition of the gene to be targeting vector and the yeast cells selectable marker; and (e) isolating the targeting vector produced by recombination between the shuttle vector and the SEF to expression targeting vector produced by recombination between the shuttle vector and the selectable marker; and (e) isolating the constitute or inserting genes or regulatory sequences into preselected or genetic loci. The method can be used for identification of the function constructs or restriction sites which results in a significant saving of time and effort in preparing targeting constructs.
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   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Fig 8; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New gene targeting vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX58236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-313353/26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raly protein sequence
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GDGGAGGIGGAST 100
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   296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INC.
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GDSSSGGGGGSSGG 222 GDGSSGGSGGASTG 14

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В
                                                                                                                                            The invention relates to a novel haematopoietic protein (HP) comprising CC an amino acid (AA) sequence of formula: RI-LI-R2; R2-LI-R1, R1-R2; or CC an amino acid (AA) sequence of formula: R1-L1-R2; R2-LI-R1, R1-R2; Or CC (R1) a modified R2 are independently selected from: (I) a modified CC (II) a modified human interleukin-3 (hIL-3) AA sequence; (III) a modified human c-mpl ligand; and a colony stimulating factor (CSF); and L1 = a CC linker capable of linking R1 to R2. This sequence represents an example CC of a linker used to construct the proteins of the invention. CC vectors comprising the nucleic acid molecules are useful for the CC vectors comprising the nucleic acid molecules are useful in CC gene therapy. The HP's are useful for stimulating the production of CC dells and for treatment of haematopoietic disorders. Disorders that CC can be treated include leukopaenia, neutropeania, aplastic anaemia and thrombocytopaenia. In vitro uses include the ability to stimulate bone marrow and blood cell activation and growth before infusion into the
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                                                         Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haematopoietic protein; human; granulocyte-colony stimulating factor; G-CSF; interleukin; c-mpl ligand; linker; gene therapy; aplastic anaemia; stem cell expansion; leukopaenia; neutropaenia; vector; bone marrow; thrombocytopaenia; blood cell activation; growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phage-derived flexible linker peptide for chimeric protein construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW17096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bauer SC,
Klein BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9712985-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-OCT-1996;
                                                                                                                                 marrow and l
                                                                                                                                                                                                                                                                                                                                                                                                                                      Multi-functional haematopoietic receptor agonists - used to stimulate the production of haematopoietic cells in patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Summers NL,
                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 33-34; 616pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SEAR ) SEARLE & CO G D.
                                                            10;
                                                                           Similarity
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Lee SC, McKe
IL, Zurfluh L;
                              GDGSSGGSGGASTG 14
   GGGSGGGSGGSEG
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                                                              Conservative
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McKearn JP,
                                                                            71.28;
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Pred. No.
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McWherter CA, Sta
                                                                 Mismatches
                                                                                            DB 18;
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                                                                                              Length 35
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RESULT 15

Search completed: August 20, 2003, 12:33:40 Job time : 31.7831 secs

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AAR79295
ID AAR7
XX AAR7
XX AAR7
                                                                                                                         A new fusion protein is disclosed which has the formula R1-L-R2, CC R2-L-R1, R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or CC variant of human interleukin-3 (hIL-3), R2 is a second colony CC variant of human interleukin-3 (hIL-3), R2 is a second colony CC thaematopoletic growth factor or IL-3 variant, and L is a linker (of CC haematopoletic growth factor or IL-3 variant, and L is a linker (of CC are shown in AAR79298-R79335 and AAR79342-R79345. The fusion protein is CC are shown in AAR79298-R79335 and AAR79342-R79345. The fusion protein is CC adoptophinant DNA techniques. Specifically claimed examples of DNA CC sequences which encode these proteins are shown in AAQ97167-Q97204 and CC gall production. It is also useful as an IL-3 antagonist or as a CC cell production. It is also useful as an IL-3 antagonist or as a CC discrete antigenic fragment for production of antibodies useful in CC growth of certain cancer cells and in treatment of astima. The fusion cCC protein can also be used to stimulate bone marrow and blood cell contracterised by decreased levels of myeloid, erythroid, lymphoid cancer cells of the haematopoletic system. The protein has the usual activity of both its component proteins, but may have increased synergistic activity and reduced undesired side effects.
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                                                            Matches
                                                                                        Query Match
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Easton AM,
Thomas JW;
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lymphokine; mutant; mutein; fusion protein; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion proteins comprising a human interleukin-3 variant, a linker and interleukin-3, a variant or a colony stimulating factor useful to increase haematopoietic cell production in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 12;
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                                                                                                                         Sequence
                                                                             Local Similarity
                               1 GDGSSGGSGGASTG
                                                              10;
GGGSGGGSEG
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Klein BK,
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                                                                                71.2%;
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McKearn JP, Olins PO,
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                                                                               Score 52;
Pred. No.
                                                                     Mismatches
                                                                                   DB 5.4;
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O, Paik K;
                                                                      4;
                                                                                                 Length 36;
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OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

4: /cgn2_6/ptodata/1

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6: /cgn2_6/ptodata/1
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Gapop 10.0 ,
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73
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   GDGSSGGSGGASTG
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/cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
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3 US-09-060-756-727

4 US-09-670-314-727

4 US-08-470-775-11

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3 US-08-169-3258-50

3 US-08-169-3258-50

3 US-08-169-324-11

4 US-08-469-124-11

5 US-08-469-124-11

6 US-08-469-318-194

6 US-08-469-318-194

7 US-08-469-318-194

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8 US-08-468-609A-195

8 US-08-468-762-27A-195

8 US-08-468-762-27A-195

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 50, Appl
50, Appl
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195, Appl
196, Appl
197, Appl
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199, Appl
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US-09-060-756-727
Sequence 727, Ag
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## ALIGNMENTS

Sequence 727, Application US/09060756 Patent No. 6183957 GENERAL INFORMATION:

APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alain

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Sequence 727, Application US/09670314

Patent No. 6492506

GENERAL INFORMATION:

APPLICANT: Cole, Stewart

APPLICANT: Cole, Stewart

APPLICANT: Buchrieser-Brosch, Roland

APPLICANT: Buchrieser-Brosch, Roland

APPLICANT: Billault, Alain

TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLECTIDE OF INTEREST FROM

TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA

TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA

TILE REFERENCE: 3495-0169

CURRENT APPLICATION NUMBER: US/09/670,314

CURRENT STLING DATE: 2001-01-12

PRIOR APPLICATION UNUMBER: 09/060,756

PRIOR FILING DATE: 1998-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SOFTWARE: PatentIn Ver. 2.; SEQ ID NO 727; LENGTH: 318; TYPE: PRT; ORGANISM: Mycobacterium s; US-09-060-756-727
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CURRENT APPLICATION NUMBER: US/09/060,756

CURRENT FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 743

SOFTMARE: Patentin Ver. 2.0
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Best Local 9
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76.9%;
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                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Co-administration of Interleukin-3
TITLE OF INVENTION: Mutants With Colony Stimulating Factors
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palan-
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                         NAME: Bennett, Dennis
REGISTRATION NUMBER: 3
                                                                                                                                                                       LENGTH:
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 GGGSGGGSEG
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Braford-Goldberg,
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71.4%;
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Patent No. 6022535
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                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                               APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                               APPLICANT:
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APPLICATION NUMBER:
                                                                                                                                               STREET: F.
STREET: F.
TITTY: Chicago
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION:
APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995
                                                                                                                  COUNTRY: U:
ZIP: 60680
                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                Illinois
Y: USA
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                                                                                                                                                                                                                                                                            Olins, Peter O.
Paik, Kumnan
                                                                                                                                                                                                                                                                                                                     Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
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Braford-Goldberg,
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                                                                                                                                                                          0. Box 5110
                                                                                                                                                                                        Corporate Patent Dept.
                                                                                                                                                                                                       Dennis A.
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                                                                                                                                                                                                                                                                                                           John P.
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               US/08/468,609A
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                      TITLE OF
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REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                ADDRESSEE: Corporate Pastreet: P. O. Box 5110
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                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                    CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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5. 6057133
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              (708)470-6501
(708)470-6881
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Klein, Barbara K.
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homas, John W.
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; MOLECULE TYPE: peptide US-08-192-325B-50
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Best Local
Matches
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              Query Match
Best Local Similarity
                                                                                                                                            TELEFAX: (708)470-688
                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                               REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C:
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/192,299
                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
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TITLE OF INVENTION: Ex-vivo expansion of hematopoietic cells using Interleukin.
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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STATE: Illinois
COUNTRY: USA
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CLASSIFICATION:
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P. O. Box 5110
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Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
                                                                                                                                                      (708)470-6881
  Conservative
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Paik, Kumnan
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                                                                                                                                                                     (708)470-6501
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Pred. No. 1
                Score 52; I
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Matches
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Patent No. 6
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                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                            APPLICANT: Abrams, APPLICANT: Bauer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P. CITY: Chicago
CITY: Illinois
TISA
   APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                    APPLICANT:
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TITLE OF INVENTION: Co-administration of Interleukin-3
TITLE OF INVENTION: Mutants With Colony Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 06-JUN CLASSIFICATION: 53(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bennett, Dennis A. REGISTRATION NUMBER: 34,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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6361977
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                                                         Braford-Goldberg,
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
                                                                                                                               Bauer, S. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Klein, Barbara K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Abrams, Mark A.
Bauer, S. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dennis A. Bennett, G.I
Corporate Patent Dept.
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N: 530
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71.4%;
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                                                                                          Sarah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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US-08-762-227A-50
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                          Sequence 50, Application US/08762227A Patent No. 6436387 GENERAL INFORMATION:
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TELEFAX: (314)737-697
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: C-TELECOMMUNICATION INFORMATION: TELEPHONE: (314)737-6986
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-FEB-1994
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CITY: Chicago
CITY: Illinois
TISA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D.
ADDRESSEE: Corporate Patent Dept.
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bennett, Dennis REGISTRATION NUMBER:
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                                                                      NUMBER OF SEQUENCES:
                                                                                                    TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
                                                      CORRESPONDENCE ADDRESS:
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ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co., Corporate Patent Dept.
STREET: P. O. Box 5110
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GY: linear
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VENTION: Multivariant IL-3
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                                                                                                                                   McKearn, John P. Olins, Peter O. Paik, Kumnan
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                                                                                                                                                                                      Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
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                                                                                                                     Thomas, John W.
                                                                                                                                                                                                                                         Braford-Goldberg,
                                                                                                                                                                                                                                                           Bauer, S.
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                                                                                                                                                                                                                                                                         Mark A.
                                                                      Fusion Protein : 197
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Pred. No.
                                                                                                                                                                                                                                         Sarah R.
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Query Match
Best Local Similarity
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                                                                                                                                      APPLICATION NUMBER: US 0
FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                        LENGTH:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/762,227A

FILING DATE: 09-Dec-1996

FILING DATE: 09-Dec-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
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LENGTH: 36 amino acids
TYPE: amino acid
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STATE: Illinois
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REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application PC/TUS9501185
                                                                                                                        36 amino acids
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                                                                   peptide
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71.2%;
71.4%;
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71.48;
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Score 52; DB Pred. No. 1.9;
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US-08-469-318-194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
             COMPUTER READABLE FORM:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
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                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                  IPPLICANT: Thomas, John W.
ITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (I
IUMBER OF SEQUENCES: 197
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.28;
Local Similarity 71.48;
es 10; Conservation
                             COUNTRY: UZIP: 60680
                                                                       STREET: P. O. CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                      ADDRESSEE:
                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                               194, Application US/08468609A
o. 6030812
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                                                                                                                                                                                                                                                                      Braford-Goldberg,
                                                                                                                                                                                                                                                                                                  Abrams, Mark A. Bauer, S. C.
                                                                                                                                                                                                                          Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
                                                                                                                                                                                                                                                                     Caparon, Maire
                                                                                                                                                                                              Paik, Kumnan
                                                                                                                                                                                                            Olins, Peter O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                      Dennis A. Bennett, G.D. Corporate Patent Dept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                        Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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                                                                                                                                                                                                                                                                                        Sarah
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                                                                                                                     Searle & Co.
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TREFERNCE (314)737-6976
TREFERNCE (314)737-6976
INFORMATION (314)737-6976
INFORMATION (314)737-6972
INFORMATION (314)737-6972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                       STREET: F.
STREET: F.
CITY: Chicago
CITY: Illinois
TTATE: IISA
                          PRIOR APPLICATION DATA:
                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                           COMPUTER READABLE FORM:
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MOLECULE TYPE:
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APPLICATION NUMBER: US 0
FILING DATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: US 08/192,325 FILING DATE: 14-FEB-1994
                                                             APPLICATION NUMBER: US/08/446,872A FILING DATE: 06-JUN-1995
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                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                        ADDRESSEE:
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Paik, Kumnan
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Klein, Barbara K.
                                                                                                                                                                                                                                                                                                                                                                                                                 McKearn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caparon, Maire H.
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Bauer, S.
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                                                                                                                                                                                                                                                                                      Dennis A. Bennett, G.D. Searle & Co.,
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06-JUN-1995
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Pred. No. 2
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Best Local Similarity
"hes 10; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-762-227A-194
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INFORMATION FOR SEQ ID
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                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION: <Unknown>
                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion Protein NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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6436387
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                                                                                NAME: Bennett, Dennis A. REGISTRATION NUMBER: 34,547
                                                                                                                                                                                                                                                                                          COMPUTER: IBM_PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                 TELEPHONE:
                                                                  REFERENCE/DOCKET NUMBER: C-2790/5
                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995
                                                                                                                                                                       APPLICATION NUMBER: US 08/192,325 FILING DATE: 14-FEB-1994
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                 TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co., Corporate Patent Dept.
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Paik, Kumnan
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Klein, Barbara K.
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Caparon, Maire H.
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                                   (708)470-6501
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71.4%;
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Pred. No. 2
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                                                                                                                                                                                                                                                                                             Version
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SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
TYPE: amino acids
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: epride
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-08-762-227A-194

Query Match
Best Local Similarity 71.4%; Score 52; DB 4; Length 49;
Best Local Similarity 71.4%; Pred. No. 2.5;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Matches 10 GGSGGGGASTG 14
Db 10 GGSGGGGGSEG 23

Search completed: August 20, 2003, 12:44:17
Job time: 10.6988 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                            d. No. 1s the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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     AAY39626
AAW16651
AAY95213
AAG65311
AAG65317
ABR01548
AAY39564
AAY02512
AAY02516
                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Anti-platelet glyc
Anti-IL-18 antibod
Anti-IL-18 antibod
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CTIA-4 VLD CDR2 re
Clone selected aft
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AAY02520 AAY02525 AAY02525 AAY02525 AAY02596 AAY02597 AAY02597 AAY02508 AAY02486 AAY02486 AAY02486 AAY02486 AAY02487 AAY02491 AAY02493 AAY02474 AAY02478	AAY02517 AAY02518
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## ALIGNMENTS

RESULT 1
AAY39626
ID AAY3

AAY39626 standard; peptide;

10 **A**A.

23-NOV-1999

(first entry)

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New binding agent comprising monomeric one complementarity determining region
                           WPI; 1999-551040/46.
                                                                                                                   10-SEP-1999.
                                                                                                                                     WO9945110-A1.
                                                                                                                                                      Synthetic.
Homo sapiens.
                                                                                                                                                                                CTLA-4; cytotoxic T-lymphocyte associated antigen 4; binding agent; VLD; variable-like domain; human; diagnosis; cancer; blood clot.
                                                                                                                                                                                                           CTLA-4 VLD CDR loop replacement.
                                            Coia G,
                                                             (DIAT-) DIATECH PTY LTD.
                                                                               06-MAR-1998;
                                                                                                 05-MAR-1999;
                                          Galanis M,
                                                                                98AU-0002210
                                                                                                 99WO-AU00136
                                             Hudson
                                             ΡJ,
                                           Irving
V-like domain in which at least loop is modified, useful for
                                             RΑ,
                                             Nuttall
                                             SD
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Example diagnosis

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6; 117pp;

English

of cancer

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    has at least one CDR (complementarity determining region) loop sequence, or part of it, modified or replaced so that, compared to unmodified VLD, its solubility is increased and/or the size is altered and/or a disulphide bond is created within, or between, one or more CDR loops. (I) are used for diagnosis, e.g. in vivo detection/localisation of cancer, blood clots etc., also in vitro when immobilised on solid supports or blosensors and therapeutically. Modified VLD may have binding affinity for drugs, steroids, pesticides, antigens, growth factors, tumour markers, cell or viral proteins. Modification of VLD improves solubility and alters binding specificity. Since VLD are derived from human proteins, the need for a humanizing step (to avoid adverse immune responses) is avoided, and modification also improves expression in
The present sequence is the heavy chain complementarity determining region 2 of an anti-cancer specific antigen human monoclonal antibody (hMAb). The hMAb can be used in medicine, e.g. clinical diagnosis of cancer or immunotherapy, or to purify cancer specific antigen. The industrial scale production of large amounts
                                                                                                  Claim
                                                                                                                                cDNA encoding human monoclonal antibody - useful in medicine, or purify cancer specific antigen
                                                                                                                                                                               WPI; 1997-275445/25
N-PSDB; AAT66783.
                                                                                                                                                                                                                                                                                                                                           15-APR-1997.
                                                                                                                                                                                                                                                                                                                                                     JP09098786-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Heavy chain; variable region; cancer specific antigen; human; monoclonal antibody; hMAb; diagnosis; cancer; immunotherapy; purification; complementarity determining region 2; CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is variable-like domain (VLD) of the human cytotoxic T-lymphocyte associated antigen 4 (CTLA-4) CDR loop replacement, used in the binding agent of the invention. The binding agent (I) comprises least one monomeric VLD that is derived from a non-antibody ligand and
                                                                                                                                                                                                                                                                               06-OCT-1995;
                                                                                                                                                                                                                                                                                                             06-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-cancer specific antigen MAb heavy chain CDR2.
                                                                                                                                                                                                                              (MOMI ) MORINAGA & CO LTD.
(SHKJ ) SHINGIJUTSU JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW16651;
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                                                                                             9; Fig 12; 7pp; Japanese.
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Pred. No.
immunotherapy, or to purify cancer scale production of large amounts
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Sequence

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RESULT 3
AAY95213
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XX AAY9
XX Vari
DT 29-2
XX Vari
COME
XX Vari
KW 91yc
KW anti
XX W COME
XX II-N
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                                                                                                            are composed of native human protein sequences and are therefore attractive potential respents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombi in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human platelet efpli alpha and of selecting a VH or VL region of an antibody that inhibits platelet aggregation are claimed. Fragments of the scFv VH or VL chain, including CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                basis of their binding to platelet GPIb. Whether displayed as surface proteins on a phagemid or secreted as free scrv by Escherichia coli, the HIb scrv clones are capable of inhibiting you willebrand factor-dependent aggregation of platelets. The synthesis of the secret of the secr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              against platelet glycoprotein Ib (GPIb). The HIb series of scFv was isolated from a human synthetic VH and VL scFv library on th basis of their binding to platelet GPIb. Whether displayed as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of complementarity determining 2 (CDR2) of the heavy chain variable region (VH) of human single chain antibody (scFv) Hib-3 (see AAY95219), which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variable heavy chain; single chain antibody; scFv; h glycoprotein Ib alpha; platelet; aggregation; antiag antithrombotic; thrombus; therapy; diagnostic; CDR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Fig 7; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibit platelet aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecule glycoprotein Ib alpha molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL/) MILLER J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-2000 (first entry)
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding anti-human platelet useful for producing antibodies which
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; antiaggregant;
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Best Local Similarity
Thehes 6; Conserv
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                                                                                                                                                                                                 The invention provides isolated antibodies, or antigen-binding portions, CC that are capable of binding to human interleukin-18 (II-18). The CC antibodies may be used to inhibit human II-18 activity in, and treat a CC disorder where II-18 is detrimental in, a human subject suffering from, CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease, CC (e.g., Huntington's chorea, Parkinson's disease, Albeimer's disease, and CC (e.g., Huntington's chorea, Parkinson's disease, Albeimer's disease, and CC (e.g., depression and schizophrenia). Treatment with an anti-II-18 CC (e.g., depression and schizophrenia). Treatment with an anti-II-18 CC (e.g., depression and schizophrenia). Treatment with an anti-II-18 CC second agent selected from an antibody, or fragment, capable of binding CC human II-12, methotrexate, anti-tumor necrosis factor, corticosteroids, CC cyclosporin, rapamycin, FK506, and non-steroidal anti-Inflammatory CC depress. The present sequence represents an anti-II-18 antibody LT28 heavy chain CDR2 fragment.
                                                                             Query Match
Best Local
                                                     Matches
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antibodies and compounds capable of binding to human interleukin-18 useful for treating, e.g., inflammatory disorders, neurological disorders, heart failure, myocardial infarction, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ghayur T,
Duncan AR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-IL-18 antibody LT28 heavy chain CDR2 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune diseases
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                                                   Similarity
6; Conser
  AISGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AISGSG 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurological;
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                                                100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91pp;
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                                                                                Score 28;
Pred. No.
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Pred. No. 61;
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                                                        Mismatches
                                                                                61;
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Shorrock CP,
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                                                                                                      Length 17;
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                                                        Indels
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Thompson JE;
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RESULT 6 ABR01548 ID ABR0

ABR01548 standard;

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RESULT 5
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Best Local S
Matches 6
                                                                                                                           inflammatory bowel disease, and osteoarthritis), neurological disorders (e.g., Huntington's chorea, Parkinson's disease, Alzhaimer's disease, and stroke), heart failure, myocardial infarction, autoimmune diseases such as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders (e.g., depression and schizophrenia). Treatment with an anti-II-18 antibody may occur before, concurrent, or after administration of a second agent selected from an antibody, or fragment, capable of binding human II-12, methotrexate, anti-tumor necrosis factor, corticosteroids, cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory agents. The present sequence represents an anti-II-18 antibody heavy chain variable region fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ghayur T,
Duncan AR,
                                                                                                                                                                                                                                                                                                             The invention provides isolated antibodies, or antigen-binding portithat are capable of binding to human interleukin-18 (IL-18). The antibodies may be used to inhibit human IL-18 activity in, and treat disorder where IL-18 is detrimental in, a human subject suffering frinflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease, inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antibodies and compounds capable of binding to human interleukin-18 useful for treating, e.g., inflammatory disorders, neurological disorders, heart failure, myocardial infarction, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           II-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.
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                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune
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                                  similarity 100 6; Conservative
 AISGSG 6
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Brocklehurst SM,
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Shorrock CP,
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Thompson JE;
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RESULT 7
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                                                                                                                                                                                                                                                                                                  The invention relates to a novel purified preparation of a human CC antibody, which binds to a tissue inhibitor of metalloprotease-[ (TIMP-1) CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of CC TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and CC a variable light chain (VLC)DR3 region. An antibody preparation of the CC invention has hepatotropic, cytostatic, nephrotropic and cardiant CC activity. The human antibody is useful for decreasing an MMP-inhibiting CC activity of a TIMP-1. It is especially useful for ameliorating the CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver CC symptoms of a disorder in which TIMP-1 is elevated, e.g. acute coronary CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon CC cancer. The antibody is also useful for detecting a TIMP-1 in a test CC elevated. The present sequence represents a VHCDR1 region of an antibody.
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                   Matches
 23-NOV-1999
                                AAY39564;
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a in which TIMP-1 is elevated, e.g. liver fibrosis, benign pros
                                                            AAY39564 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; acute coronary syndrome; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypertrophy or lung cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FARB ) BAYER CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lupus nephritis; glomerulosclerotic renal disease; lung cancer; VHCDR1;
                                                                                                                                                                                                   Local Similarity nes 6; Conserv
                                                                                                                                                                     1 AISGSG 6
                                                                                                                                                                                                                                                                                              invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Knorr AM, Schauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Page 47;
                                                                                                                                         AISGSG
                                                                                                                                                                                                                                                                  17 AA;
                                                                                                                                                                                                     Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΑG
                                                           peptide;
                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228pp; English.
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                                                                                                                                                                                                   0,
                                                              25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #1
                                                                                                                                                                                                                  Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hirth-dietrich C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              benign prostate hypertrophy; colon cancer
                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                0B
61;
                                                                                                                                                                                                                              24;
                                                                                                                                                                                                   0;
                                                                                                                                                                                                                             Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    benign prostate
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kraft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ß
                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krebs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorder
                                                                                                                                                                                                Gaps
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RESULT 8
AAV02512
ID AAVX
XX
AC AAVC
XX
AC AAVC
XX
DT 15-J
DT 15-J
XX
DE Clon
XX
DE Clor
XX
DE CRIP
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DE CRIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               has at least one CDR (complementarity determining region) loop sequence, or part of it, modified or replaced so that, compared to unmodified VLD, its solubility is increased and/or the size is altered and/or a disulphide bond is created within, or between, one or more CDR loops. (I) are used for diagnosis, e.g. in vivo detection/localisation of cancer, blood clots etc., also in vitro when immobilised on solid supports or blosensors and therapeutically, modified VLD may have binding affinity for drugs, steroids, pesticides, antigens, growth factors, tumour markers, cell or viral proteins. Modification of VLD improves solubility and alters binding specificity. Since VLD are derived from human proteins, the need for a humanizing step (to avoid adverse immune responses) is avoided, and modification also improves expression in
                                                         Synthetic
                                                                                                            enrichment;
                                                                                                                                                                                             Clone selected after
                                                                                                                                                                                                                                                      15-JUL-1999
                                                                                                                                                                                                                                                                                                         AAY02512
                                                                                                                                                                                                                                                                                                                                                                AAY02512 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is a variant of the CDR2 of the variable-like domain (VLD) of the human cytotoxic T-lymphocyte associated antigen 4 (CTLA-4), used in the binding agent of the invention. The binding agent (I) comprises at least one monomeric VLD that is derived from a non-antibody ligand and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         one complementarity determining diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 18; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New binding agent comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-551040/46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DIAT-) DIATECH PTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9945110-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTLA-4 VLD CDR2 region variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AISGSG 14
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                                                                                                          functional polypeptide;
; single chain antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98AU-0002210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                          panning a NNK library of the invention
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ing region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Irving RA,
                                                                                                            ligand; non-functional;
ScFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V-like domain in which at least loop is modified, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          рв
89;
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WO9920749-A1

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RESULT 9
AAY02516
ID AAY0
XX AAY0
AC AAY0
DT 15-J
XX Clon
XX Scre
KW Scre
KW Scre
KW Scre
KW Scre
KW Synt
XX S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting a repertoire of polypeptides with a generic ligand, and then screening selected functional polypeptides with a target ligand. The method permits the removal from a chosen repertoire of polypeptides, those which are non-functional, e.g. as a result of the introduction of frame-shift mutations, stop codons, folding mutants or expression mutants which would be or are incapable of binding to any target ligand. The method also permits the enrichment of a chosen repertoire of polypeptides for those polypeptides which are functional, well folded and highly expressed. The polypeptides which are functional, well folded and highly expressed. The polypeptides obtained can be used in libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 6
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20-OCT-1997;
13-NOV-1997;
                                                                         21-NOV-1997;
20-OCT-1997;
13-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-APR-1999
                                                                                                                                                                                                                                                                              W09920749-A1
                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                 Screening; functional polypeptide; ligand; enrichment; single chain antibody; ScFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone selected after panning a NNK library of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY02516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY02516 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; F1g 4;
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                          (MEDI-) MEDICAL RES COUNCIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AISGSG 6
||||||
AISGSG 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for functional polypeptides which bind a ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Winter
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97GB-0022131.
97US-0065428.
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97GB-0022131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                         non-functional;
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RESULT 10
AAY02517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting a repertoire of polypeptides with a generic ligand, and then screening selected functional polypeptides with a target ligand. The method permits the removal from a chosen repertoire of polypeptides, those which are non-functional, e.g. as a result of the introduction of frame-shift mutations, stop codons, folding mutants or expression mutants which would be or are incapable of binding to any target ligand. The method also permits the enrichment of a chosen repertoire of polypeptides for those polypeptides which are functional, wall folded and highly expressed. The polypeptides which are functional, wall folded and highly expressed. The polypeptides obtained can be used in capresent clones selected after panning primary and somatic NNK libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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                                                                                                                                                                                                 21-NOV-1997;
20-OCT-1997;
13-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomlinson
The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting repertoire of polypeptides with a generic ligand, and then screen
                                                                                                                                                                                                                                                                                                            WO9920749-A1
                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                    Screening; functional polypeptide; ligand; non-functional; enrichment; single chain antibody; ScFv.
                                                                                                                                                                                                                                                                                                                                                                                                            Clone selected after panning a NNK library of the invention
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                                                                                    Screening
                                                                                                               WPI; 1999-288302/24
                                                                                                                                           Tomlinson I,
                                                                                                                                                                                                                                                        20-OCT-1998;
                                                                                                                                                                                                                                                                                    29-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIP-BSA and hen egg lysozyme).
                                                          Example 3;
                                                                                                                                                                       (MEDI-) MEDICAL RES COUNCIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig 4; 67pp; English.
                                                          Fig 4; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                           Winter
                                                                                    functional polypeptides which bind a ligand
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97GB-0022131.
97US-0065428.
                                                                                                                                                                                                                                                        98WO-GB03135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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Pred. No.
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screening

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RESULT 11
AAY02518
The specification describes a method for screening for functional CC polypeptides which bind a ligand. The method comprises contacting a CC repertoire of polypeptides with a generic ligand, and then screening CC selected functional polypeptides with a target ligand. The method CC permits the removal from a chosen repertoire of polypeptides, those CC which are non-functional, e.g. as a result of the introduction of frame-shift mutations, stop codons, folding mutants or expression mutants which would be or are incapable of binding to any target tand. The method also permits the enrichment of a chosen repertoire weppeptides for those polypeptides which are functional, well folded by expressed. The polypeptides obtained can be used in a grophylactic and therapeutic procedures. ANY02473-Y02525 and tigens (bovine ubiquitin, rat BIP, bovine histone,
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20-OCT-1997;
13-NOV-1997;
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                                                                                                                                                                                                                                                                                                   Screening
                                                                                                                                                                                                                                                                 Example 3; Fig 4; 67pp; English.
                                                                                                                                                                                                                                                                                                                                     WPI; 1999-288302/24.
                                                                                                                                                                                                                                                                                                                                                                    Tomlinson I,
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                               for functional polypeptides which bind a ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      functional polypeptide; ligand; non-functional;
; single chain antibódy; ScFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 AA;
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97GB-0022131.
97US-0065428.
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RESULT 1:
AAY02520
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Matches 6; Conserv
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20-OCT-1997;
13-NOV-1997;
                                                                                 ligand. The method also permits the enrichment of a chosen repertoire of polypeptides for those polypeptides which are functional, well fold and highly expressed. The polypeptides obtained can be used in diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525 represent clones selected after panning primary and somatic NNK libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
                                                                                                                                                         The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting a repertoire of polypeptides with a generic ligand, and then screening selected functional polypeptides with a target ligand. The method permits the removal from a chosen repertoire of polypeptides, those which are non-functional, e.g. as a result of the introduction of frame-shift mutations, stop codons, folding mutants or expression mutants which would be or are incapable of binding to any target
                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening; functional polypeptide; ligar enrichment; single chain antibody; ScFv.
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Similarity 6; Conserv
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                                                 56 AA;
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                                                                                                                                                                                                                                                                                                    functional polypeptides which bind a ligand
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97GB-0022131
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           100.0%;
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                                                                         Lysozyme).
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           Score 28;
Pred. No.
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Pred. No.
 Mismatches
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             2e+02;
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1 AISGSG 6 |||||| 6 AISGSG 1

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RESULT 14
AAY02524
ID AAY02
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AC AAY02
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DT 15-JU
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DE Clone
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AAY02522
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                                                                                                                                                                   Query Match
Best Local Similarity
6; Conserve
                                                                                                                                                                                                                              The specification describes a method for screening for functional copypeptides which bind a ligand. The method comprises contacting a crepertoire of polypeptides with a generic ligand, and then screening selected functional polypeptides with a target ligand. The method permits the removal from a chosen repertoire of polypeptides, those which are non-functional, e.g. as a result of the introduction of trame-shift mutations, stop codons, folding mutants or expression mutants which would be or are incapable of binding to any target ligand. The method also permits the enrichment of a chosen repertoire of polypeptides for those polypeptides which are functional, well folded and highly expressed. The polypeptides which are functional, well folded and highly expressed. The polypeptides obtained can be used in capable tichnes selected after panning primary and somatic NNK libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone, NYC)
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20-OCT-1997;
13-NOV-1997;
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Clone selected after panning a NNK library of the invention
                        15-JUL-1999
                                                AAY02524;
                                                                     AAY02524 standard; Protein;
                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for functional polypeptides which bind a ligand
                                                                                                                                                                                                                              56 AA;
                                                                                                                                                                              Conservative
                       (first entry)
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97GB-0022131.
97US-0065428.
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Pred. No. 2e+02;
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RESULT 15
AAY02525
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AC AAY0;
DT 15-JI
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                                                                      Synthetic.
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The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting a repertoire of polypeptides with a generic ligand, and then screening selected functional polypeptides with a target ligand. The method permits the removal from a chosen repertoire of polypeptides, those which are non-functional, e.g. as a result of the introduction of frame-shift mutations, stop codons, folding mutants or expression mutants which would be or are incapable of binding to any target ligand. The method also permits the enrichment of a chosen repertoire of polypeptides for those polypeptides which are functional, well folded and highly expressed. The polypeptides which are functional, well folded diagnostic, prophylactic and therapeutic procedures. ANYO2473-Y02525 represent clones selected after panning primary and somatic NNK libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone, where the polypeptides which are functional to the polypeptides with 5 antigens (bovine ubiquitin, rat BIP, bovine histone, where the polypeptides with 5 antigens (bovine ubiquitin, rat BIP, bovine histone).
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20-OCT-1997;
13-NOV-1997;
                                                                                                                                         Screening; functional polypeptide; enrichment; single chain antibody;
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                                                                                                                                                                                              Clone selected after panning a NNK library of the invention
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20-OCT-1998;
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6; Conserv
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ilarity 100.0%;
Conservative
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97GB-0022131.
97US-0065428.
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 98WO-GB03135
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Pred. No. 2e+
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ScFv.
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Search completed: August 20, 2003, 12:33:41 Job time: 14.1928 secs
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                                                                                                                                                                                                                           The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting a crepertoire of polypeptides with a generic ligand, and then screening selected functional polypeptides with a target ligand. The method permits the removal from a chosen repertoire of polypeptides, those which are non-functional, e.g. as a result of the introduction of frame-shift mutations, stop codons, folding mutants or expression cmutants which would be or are incapable of binding to any target ligand. The method also permits the enrichment of a chosen repertoire cof polypeptides for those polypeptides which are functional, well folded and highly expressed. The polypeptides obtained can be used in crepresent clones selected after panning primary and somatic NNK clibraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone, with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative 0;
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20-OCT-1997;
13-NOV-1997;
                                                                                                                                                                                                                         Sequence
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97GB-0022131.
97US-0065428.
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Perfect s Sequence:

OM protein

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Minimum

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2, Appli 8170, Ap

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24, Appl 5229, Ap 6222, Ap 6222, Ap 6222, Ap 17011, A 17011, A 17011, A 11, Appl 14, Appl

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Total number
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen
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/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
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               2 US-08-428-197-48
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3 US-08-983-607-36
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5 PCT-US93-10555-2
5 US-08-983-607-46
2 US-08-983-607-22
4 US-08-983-607-22
5 US-08-983-607-22
6 US-08-983-607-23
6 US-08-983-607-38
6 PCT-US93-10555-38
7 US-08-983-607-28
8 US-09-252-991A-20646
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68, Appl
69, Appl
51, Appl
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                                                                                                                                  TYPE: amino a TOPOLOGY: lir MOLECULE TYPE: US-08-428-197-48
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US-08-428-197-48
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                                            Query Match
Best Local S
Matches 6
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/
EILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:

NAME: Howells, Stacy L.

REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2
REFERENCE/TOKIET NUMBER:
                                                                                                                                                                                                                                         TELEFAX: (619) 455-511
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: WETHOD FOR
TITLE OF INVENTION: VARIABLE R.
TITLE OF INVENTION: VACCINATIO
TITLE OF INVENTION: THEREOF
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CITY: Los Angeles
STATE: California
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GY: linear
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1880 Century Park East - Suite 500
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ilarity 100.0%;
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US-09-388-354-24

US-08-887-534A-24

US-09-527-431-24

US-09-134-001C-5229

US-09-117-532A-6222

US-08-311-731A-28

US-09-252-991A-20578

US-09-252-991A-17011

US-08-461-990B-11

US-08-461-990B-11

US-08-461-990B-11

US-08-6613-729A-14

US-08-465-72-14

US-08-465-72-14

US-08-643-563A-14

US-08-643-563A-14
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                                                                     Score 28;
Pred. No.
                                                 Mismatches
                                                                     DB 2;
1.6e+02;
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PCT-US93-10555-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48, Application PC/TUS9310555 GENERAL INFORMATION:
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COMPUTER READABLE FORM
                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                      APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE, DOCKET NUMBER: FD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                             TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                          UMBER OF SEQUENCES:
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FILING DATE: 29-OCT-1993
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1880 Century Park East - Suite
                                  USA
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Pred. No.
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US-08-428-197-2
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       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB
FILING DATE: June 28, 1996
                                                                                                     OPERATING SYSTEM: MS DOS SOFTWARE: Word Processing CURRENT APPLICATION DATA:
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US9:
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-
                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                              STREET:
                                                                    APPLICATION NUMBER: US/08/9 FILING DATE: April 27, 1998
                                                          CLASSIFICATION:
                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                  COUNTRY: United ZIP: 06520-8114
CLASSIFICATION:
                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                               Connecticut
United States of America
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                                                                                                                                                                                                                                                                                        Department of Molecular Biophysics
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                            PCT/IB96/01032
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                                                                                       US/08/983,607
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Pred. No. 1.9e+0
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 INDEPENDENT (619) 455-5100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 aming
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GENERAL INFORMATION:
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Best Local S
                                                                                  APPLICATION NUMBER: PCT/US93/
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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DESCRIPTION: polypeptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
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ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: DM414 scFv antibodies obtained from LIBRARY: fUSE5 fusion phage construct CLONE: V474
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REGISTRATION NUMBER:
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Similarity 100.0%;
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amino acid
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1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                  USA
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VENTION: METHOD FOR STIMULATING PRODUCTION OF
VENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
VENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
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29-OCT-1993
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Pred. No. 1.
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                                      Query Match
Best Local Similarity
"~+~hes 6; Conserva
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US-08-545-809A-109
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 117 amino acid
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/545,809A FILING DATE: 27-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Honjo, Ta
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                                                                                                                                                                                                     TELEPHONE: 617-542-8906
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OPERATING SYSTEM: Windows
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                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                  NAME: Freeman, John W
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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69 AISGSG
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SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
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Pred. No.
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Pred. No.
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RESULT 8
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US-08-983-607-46
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: OSbourt
APPLICANT: Allen,
                                                 Sequence 12, Application US/08652816A Patent No. 5872215
                                                                                                                                                                                                                           Query Match
Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       LIBRARY: VH antibodies obtained LIBRARY: fusion phage construct CLONE: C55
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MEDIUM TYPE: 3.5" 1.44 Mb diskette
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APPLICANT: Xiaohong Cai
                                                                                                                                                                                                          Local Similarity
nes 6; Conserv
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FILING DATE: April 27, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MARY M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University STREET: 266 Whitney Avenue
                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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cytes
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Pred. No.
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                                                                                                                                                                                                                                        Length 117
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                                                                                                                                       RESULT 9
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                                                                                    Sequence 22, Application US/08983607 Patent No. 6140470
                                                                  Patent No. 6140470 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Hum
TITLE OF INVENTION: bod
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/652,816A FILING DATE: 23-MAY-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1:25 (EPO) CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                         Local Similarity tes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/
FILING DATE: 02-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: GB 9610824.6 FILING DATE: 23-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                            118 amino acids
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Conservative
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/ENTION: Specific binding members, materials
                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                               312-474-6300
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24-MAR-1992
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23-SEP-1992
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   bodies
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                   Human Anti-Tumor Monoclonal Anti-
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Pred. No.
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; NAME/KEY: heavy chain US-08-983-607-22
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38,
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                                                                                                                                                                                                                                                                                                       APPLICANT: Knapp1
                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word Processing CURRENT APPLICATION DATA:
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APPLICATION NUMBER: FILING DATE: June 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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DESCRIPTION:
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                                                                                                          FITLE OF INVENTION:
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INDIVIDUAL ISOLATE: peripheral blood lymphocytes
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ORGANISM: nized with autologous tumor cells)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50
                                                                   ANT: Moroney, Simon
ANT: Plueckthun, Andreas
DF INVENTION: Protein/(Poly)peptide libraries
OF SEQUENCES: 373
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N: 435
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F. Haley, Jr., Esq. c/o Fish & Neave
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Pred. No.
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US-09-025-769B-63
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                    ALP: 1002.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
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COMPUTER: IBM PC COMPATIBLE
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
                      SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION UNMER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
APPLICATION UNMER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
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FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
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TOPOLOGY: linear
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STATE: New York
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5. 6300064
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Plueckthun, Andreas
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Pred. No.
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NAME: James F. Haley, REGISTRATION NUMBER: 2

, Jr., 1 27,794

Esq.

MORPHO/5

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RESULT 13
US-08-428-197-38
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                                                                                                                  Matches
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Pope, AI
APPLICANT: Pritchai
APPLICANT: William
APPLICANT: Johnson
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Best Local :
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APPLICATION NUMBER: US 60/028,897

FILING DATE: 21-0CT-1996

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 122 amino acids
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                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/958,201
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CITY: Chicago
Illinois
TTATE: Illinois
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TOPOLOGY: lin-
WOLECHTP
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CLONE: 2G
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                Similarity 6; Conserv
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5977319
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                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams, Andrew J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pritchard,
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                                                                                                                            Score 28;
Pred. No.
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Pred. No.
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2e+02;
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Query Match
Best Local Similarity
"">+"hes 6; Conserv
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PCT-US93-10555-38
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
FILING DATE: 29-OCT-1993
ATTORNEY_AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                       STREET: 100
CITY: LOS Angeles
STATE: California
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                ADDRESSEE:
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STATE: California
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STREET: 1880 Century Park East - Suite 500
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                                                                          90067
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1880 Century Park East - Suite 500
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; TOPOLOCY: linear
; MOLECULE TYPE: protein
PCT-US93-10555-38
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US-08-983-607-51
                                                                                  CURRENT APPLICATION.

APPLICATION NUMBER: US/08/983, bv,
FILING DATE: APril 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/1896/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MATY M. KLINSKY
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 203-773-9544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                        TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 455-5110 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: FD TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/
FILING DATE: 29-OCT-1993
CLASSIFICATION:
 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Department of Molecular Biophysics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TY: New Haven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 AISGSG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AISGSG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RY: United States of America 06520-8114
                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08983607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 Whitney Avenue
                                     124 residues
                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC
single
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; NAME/KEY: heavy chain US-08-983-607-51
Search completed: August 20, 2003, 12:44:18 Job time: 5.15663 secs
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                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                   LIBRARY: VH antibodies obtained from fUSE5
LIBRARY: fusion phage construct
CLONE: E-13
                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE: peripheral blood lympho-
INDIVIDUAL ISOLATE: cytes
                                                                50 AISGSG 55
                                                                                                1 AISGSG 6
                                                                                                                              100.0%;
milarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (melanoma patient immunized with autologous tumor cells)
                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide
                                                                                                                                 Score 28; DB
Pred. No. 2e+
0; Mismatches
                                                                                                                                                                    DB 3; Length 124;
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Title:
Perfect score:
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No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
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                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                               Score
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28
1 AISGSG 6
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Match Length
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100.0
100.0
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100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
) /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
) /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
) /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
) /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
| /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
| /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
| /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
| /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
| /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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              ВВ
9 US-09-192-854-10

10 US-09-968-561A-38

10 US-09-968-561A-38

10 US-09-968-561A-68

10 US-09-968-561A-80

10 US-09-968-561A-80

10 US-09-968-561A-92

10 US-09-968-561A-122

10 US-09-968-561A-122

10 US-09-968-561A-134

10 US-09-968-561A-134

10 US-09-968-561A-146

10 US-09-968-561A-146
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       Sequence 27, Appl
Sequence 10, Appl
Sequence 14, Appl
Sequence 38, Appl
Sequence 68, Appl
Sequence 74, Appl
Sequence 80, Appl
Sequence 12, Appl
Sequence 122, Appl
Sequence 124, Appl
Sequence 134, App
Sequence 146, App
Sequence 146, App
Sequence 146, App
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12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	11	10	10	10	10	10	10	10	10	10	10	10
-09-968-744A-	68-744A-	-09-968-744A-	-09-968-7	-09-968	-09-968	-968	US-09-968-744A-140	896-60-	9-968	9-968	8	-09-968	9-968	8	-968	-09-968	<b>-968</b>	US-09-972-656-45	9-968-561	9-968-561	9-968-561#	-09-968-561A	-09-968-561	-09-968-561A	-09-968-561A	-09-968-5612	-968-561#	-09-968-561	US-09-968-561A-194
260,	236,	218,	212,	194,	e 188,	146,	Sequence 140, App	e 134,	128,	122,	92,	86,	, 08	74,	68,	е 38,	14,	Ø	e 314	308	e 296	e 284	e 272	e 266	e 260,	236,	218,	Sequence 212, App	•

### ALIGNMENTS

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; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B; OTHER INFORMATION: antibody clone US-09-300-425B-27
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US-09-300-425B-27
                                                                                                                                                                                                                                                                         SOFTWARE: F
SEQ ID NO 27
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                            Matches
                                                                                                                                                                                                                                                                                                                               APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VIII, Francesca
APPLICANT: BIRCHLER, Manfired
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
NUMBER: OF SEQ ID NOS: 34
                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                     1 AISGSG 6
1 AISGSG
                                                                          Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                PatentIn Ver. 2.1
                                                                            Conservative
                                                                                             100.0%;
                                                                              0:
                                                                          Score 28; DB 11;
Pred. No. 4.5e+05;
; Mismatches 0;
                                                                                                                  Length 6;
                                                                              Indels
                                                                              0;
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RESULT

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                                                                         US-09-968-561A-38
                                                                                          RESULT 4
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US-09-968-561A-14
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US-09-968-561A-14
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                     GENERAL INFORMATION:
                                    Sequence 38, Application US/09968561A Patent No. US20020164642A1
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: P
SEQ ID NO 14
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                             Query Match
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Best Local Similarity' 100.0%;
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LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.0
APPLICANT:
                                                                                                                                                                                                                                                                                                                                    LENGTH: 17
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/968,561A CURRENT FILING DATE: 2001-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tomlinson, Ian MAPPLICANT: Winter, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Winter, Greg
APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods
FILE REFERENCE: 3789/72916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: GB 9722131.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                AISGSG 6
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Tomlinson, Ian M
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                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                     100.0%; Score 28; 100.0%; Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                         10; Length 17;
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; ORGANISM: Homo sapiens US-09-968-561A-68
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Best Local S
Matches 6
                                                                                                                                                                                                                             SOFTWARE: P
                                                                           Matches
                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
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TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
FILE REFERENCE: 8039/1073B
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
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PRIOR APPLICATION NUMBER: US 09/511,939
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
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TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
FILE REFERENCE: 8039/1073B
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RESULT 6 US-09-968-561A-74 ; Sequence 74, Application US/09968561A

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US-09-968-561A-80
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US-09-968-561A-74
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PRIOR FILING DATE: 1997-10-20
PRIOR FILING DATE: 1997-11-30
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
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Matches 6
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TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
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APPLICANT: Winter, Gregory
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APPLICANT: Winter, Gregory
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TYPE: PRT
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ITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
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TTLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
ILE REFERENCE: 8039/1073B
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US-09-968-561A-86
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                                                                                     ; ORGANISM: Homo sapiens US-09-968-561A-92
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PRIOR FILING DATE: 1997-10-20

PRIOR PPLICATION NUMBER: US 60/065,248

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: US 60/066,729

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: PCT/GB98/03135

PRIOR FILING DATE: 1998-10-20

PRIOR FILING DATE: 1998-10-20
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Best Local :
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TITLE OF INVENTION: Method to Screen Phage Display Libraries
FILE REFERENCE: 8039/1073B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
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PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
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APPLICANT: Winter, Gregory
TITLE OF INVENTION: Wethod to Screen Phage Display Libraries with Different Ligand
FILE REFERENCE: 8039/1073B
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US-09-968-561A-128
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                                          Query Match
                                                                                                                                                              SEQ ID NO 128
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      Matches
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Best Local :
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PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
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CURRENT FILING DATE: 2001-10-01
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TIFLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
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TYPE: PRT
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TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
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APPLICATION NUMBER: US 60/065,248
FILING DATE: 1997-11-13
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US-09-968-561A-134
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JS-09-968-561A-140
                                                                                  SEQ ID NO 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 140, Application US/09968561A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 134, Application US/09968561A
Patent No. US20020164642A1
                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: GB 9722131.1 PRIOR FILING DATE: 1997-10-20 PRIOR APPLICATION NUMBER: US 60/065,248 PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
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                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 8039/1073B
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/GB98/03135 PRIOR FILING DATE: 1998-10-20
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
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TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
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                   ORGANISM: Homo sapiens
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                                                                                                                                                                  APPLICATION NUMBER: US 09/511,939
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US-09-968-561A-188
; Sequence 188; Application US/09968561A
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                                                                              CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR EILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US/06/03135
PRIOR APPLICATION NUMBER: US/09/511,939
PRIOR APPLICATION NUMBER: US/09/511,939
PRIOR APPLICATION NUMBER: US/09/511,939
PRIOR APPLICATION NUMBER: US/09/511,939
PRIOR FILING DATE: 2000-02-24
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US-09-968-561A-146
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SOFTWARE: Paten
SEQ ID NO 146
LENGTH: 17
TYPE: PRT
SOFTWARE: Pat
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LENGTH: 17
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TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
CURRENT APPLICATION UNMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: G50/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: DCT/GB98/03135
PRIOR FILING DATE: 1997-10-20
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Best Local Similarity 100.0%;
Matches 6; Conservative 0;
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APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
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NUMBER OF SEQ ID NOS:
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tent No. US20020164642A1
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Pred. No.
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; ORGANISM: Homo sapiens US-09-968-561A-188
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Query Match 100.0%; Score 28; DB 10; Length 17; Best Local Similarity 100.0%; Pred. No. 28; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps
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Search completed: August 20, 2003, 13:16:45
Job time: 7.50602 secs

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Title: Perfect score: Sequence: Total number of hits satisfying chosen parameters: OM protein - protein search, using sw model Searched: Scoring table: Run on: BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-512-082-27 28 1 AISGSG 6 August 20, 2003, 12:25:56; Search time 4.19277 Seconds (without alignments)
137.621 Million cell updates/sec 283308 seqs, 96168682 residues GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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# ALIGNMENTS

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RESULT 5
S24260
                                                                              Ig heavy chain V region (VH26-DA1-JH4) - human C;Species: Homo sapiens (man) C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #t C;Accession: S24260 R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, submitted to the EMBL Data Library, June 1992
   A; Molecule
                               A;Description: A single VH
A;Reference number: S24247
A;Accession: S24260
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submitted to the EMBL Data
A;Description: A single VH
A;Reference number: S24247
A;Accession: S24257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region (VH26-DXP1-JH4) - human C;Species: Homo sapiens (man) C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change C;Accession: S24257
                     A;Status:
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A;Molecule type: DNA
A;Residues: 1-100 <STE>
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C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S24258
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Species: Homo sapiens (man)
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e type: DNA
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RESULT
S24249
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C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;10-92/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, A; Description: A single VH gene pred
                                                                                                                                                                                                                                                                                                                                    C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
C;Accession: S24249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X67063
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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A; Cross-references: EMBL:X67068
A; Cross-references: EMBL:X67068
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 5-87/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-105 <STE>
                                                                                                                                                                                                                                                A; Reference number: A; Accession: S24249
                                                                                                                                                                                                                                                                  A; Description: A single VH
A; Reference number: S24247
                                                                                                                                                                                                                                                                                                                   R; Stewart, A.K.; Huang, C.; Stollar, B.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S24247
A; Accession: S24255
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                       C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F; 2-84/Domain:
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submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region (VH26-DLR5-JH4) - human
C; Species: Homo sapiens (man)
C; Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region
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A; Residues: 1-104 <STE>
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Best Local Similarity
Matches 6; Conserv
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Best Local
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                                                                Similarity 6; Conserv
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49
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Pred. No.
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Pred. No.
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C;Accession: PH1648
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1648
A;Accession: PH1642; MUID:93301610; PMID:8315388
A;Residues: 1-108 <HIL>
A;Residues: 1-108 <HIL>
A;Experimental source: B cell
C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin
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A;Residues: 1-106 <STE>
A;Cross-references: EMBL:X67064; NID:g38385; PIDN:CAA47449.1; PID:g38386
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;4-86/Domain: immunoglobulin homology <IMM>
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submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates i
A;Reference number: S24247
A;Accession: S24256
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A; Molecule type: DNA
A; Residues: 1-106 <STE
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                                                            A; Molecule type: mRNA
A; Residues: 1-109 <HIL>
A; Residues: 1-109 <HIL>
A; Experimental source: B cell
C; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
E; 7-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                        R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1649
                                                                                                                                                                                                                                                                                                Ig heavy chain V region (clone 2E7) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1649
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C; Species: Homo sapiens (man)
C; Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
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PH1648
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Llarity 100.0%;
Conservative 0
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Pred. No. 38;
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  Score 28;
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  R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Sci
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates:
A;Reference number: S24247
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A;Molecule type: DNA
A;Residues: 1-109 <STE>
A;Cross-references: EMBL:x67062
A;Cross-references: EMBL:x67062
C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin C;Keywords: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                            C;Superfamily: immunoglobulin V region; im
C;Keywords: heterotetramer; immunoglobulin
F;12-94/Domain: immunoglobulin homology <I
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region (VH26-DLR4-JH6) - human C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change C;Accession: S24253
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                Ig heavy chain V region (VH26-DN1-JH4) -
C; Species: Homo sapiens (man)
C; Date: 19-Feb-1994 #sequence_revision 10
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 C; Accession:
                                                                   S24250
                                                                                 RESULT 13
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                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-109 <STE>
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R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1647
A;Molecule type: mRNA
A;Residues: 1-112 <HIL>
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                                                                                                                                                           A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region (clone 2D10) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1647
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Best Local Similarity
Watches 6; Conserve
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A;Cross-references: EMBL: 233401
C;Superfamily: immunoglobulin V region; immunoglobulin homology F;15-98/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of mult:
A;Reference number: 869909; MUID:94335315; PMID:8057663
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A;Cross-references: EMBL:X67071
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-110 <STE>
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A; Status: preliminary
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Search completed: August 20, 2003, 12:42:15

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1 AISGSG 6
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Match
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  SwissProt_41:*
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AMI1_MYCTU
SLAP_BACSH
PROC_PSEAE
BACH_HALHP
LAVI_PHYPO
SPYA_RABIT
SVPI_CAVPO
ODP2_STAAU
DHE4_UNIT
DHE4_SALTY
PRIA_THEMA
PQGI_EOOLI
BA2A_MOUSE
PGCA_BOVIN
                                                                                                                                                                                                                                           PROC_MYCTU
DHAS_STRAK
DHAS_CORFL
DHAS_CORFL
GUN4_TRIRE
DHAS_MYCBO
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Q48315
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Q11141
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4 mycobacteri
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0 oryctolagus
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1 staphylococ
7 unknown pro
6 salmonella
1 salmonella
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7 bacillus sp
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HV3C_HUMAN
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P01764;

P01764;

21-JUI-1986 (Rel. 01, Created)

21-JUI-1986 (Rel. 01, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15 d heavy chain V-III region VH26 precursor.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]
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MEDLINE-81101090; PubMed-6450418;

Matthyssens G., Rabbitts T.H.;

Matthyssens G., Rabbitts T.H.;

Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
    1 AISGSG
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immunoglobulin

26 92.9 241 1 LEG3_RABIT 26 92.9 249 1 LEG3_HUMAN 26 92.9 269 1 MTN_TREPA 26 92.9 269 1 MTN_TREPA 26 92.9 295 1 LEG3_CANFA 26 92.9 315 1 GBF1_ARATH 27 92.9 315 1 GBF1_HUMAN 28 92.9 372 1 GDF1_HUMAN 29 92.9 373 1 LS2_ADE12 20 92.9 373 1 LS2_ADE12 21 92.9 374 1 DF3_STRCO 22 92.9 375 1 DF3_STRCO 23 92.9 376 1 DF3_STRCO 24 92.9 376 1 DF3_STRCO 25 92.9 376 1 DF3_STRCO 26 92.9 376 1 DF3_STRCO 27 92.9 376 1 DF3_STRCO 28 92.9 376 1 DF3_STRCO 29 92.9 376 1 DF3_STRCO 29 92.9 376 1 DF3_STRCO 20 92.9 376 1 DF3_STRCO 21 DF3_STRCO 22 P27903 streptomyce 23 P28024 drosophila 24 P28025 drosophila 25 P2.9 462 1 CHI1_CANAL 26 P2.9 462 1 CHI1_CANAL 27 P28026 candida alb
241 1 LEG3_RABIT 249 1 LEG3_HUMAN 249 1 LEG3_HUMAN 249 1 MIN_TREPA 249 1 MIN_TREPA 250 1 LEG3_CANFA 251 1 LEG3_CANFA 251 1 GBF1_ARATH 2573 1 L52_ADB12 258 1 L52_ADB12 258 1 DP3B_STRCO 258 278 279 27903 276 1 DP3B_STRCO 259 21
1 LEG3_RABIT P47845 1 LEG3_HUMAN P17931 1 MTN_TREPA P96122 1 LEG3_CANEPA P38886 1 GBF1_HUMAN P27339 1 L52_ADE12 P3774 1 GDF1_HUMAN P27393 1 L52_ADE12 P36715 1 DP3B_STRCO Q92196 1 DAR_RHIME Q92196 1 DAR_RHOUGR P00369 1 DH64_NEUCR P00369
P47845 P17931 P96122 P98486 P42774 P27539 P56715 P27903 Q921p6 P83294 P00369 P46876
P47845 P17931 P96122 P98486 P42774 P27539 P56715 P27903 Q921p6 P83294 P00369 P46876
P47845 c P17931 h P96122 t P38486 c P42774 a P27739 h P277903 s P27903 s P36715 h P36715 h P36715 h P369296 d P83296 d P83296 d P83369 n

### ALIGNMENTS

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Hypothetical protein AF1796.
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Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
                                                                                                                                                                                   028478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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28-FEB-2003 (Rel. 41,
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           Smith D.R., Doucette-Stamm I.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Oiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum
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                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum. Archaea; Euryarchaeota; Methanobacteria;
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Nature 390:364-370(1997).
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                                                                                                                                                                                                                                                                                  Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sokine M., Baba S.-I., Ankai A., I Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Wakamura Y., Nomura N., Sako Y., Kikuchi H.;

"Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Ki.";

DNA Res. 6:83-101(1999).
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SEQUENCE 1
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                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99310339;
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-K1
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Crenarchaeota; Thermoprote1;
Desulfurococcaceae; Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aeropyrum pernix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical APE1940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9YAKO;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001347; SIS. Pfam; PF01380; SIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YJ40_AERPE
                                                                                                                             EMBL; AP000062; BAA80949.1;
                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                      Hypothetical
                                                                                    Pfam; PF01380; SIS; 1.
                                                                                                   interPro;
                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE SIS FAMILY. YCKF SUBFAMILY.
                                                                                                 H72582; H72582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conserv
6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 AA; 2
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100.0%;
llarity 100.0%;
Conservative (
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                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                PubMed-10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Complete proteome.
21570 MW; 9840D27964B6F267 CRC64;
                                                         1; Complete 24339 MW;
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Pred. No.
 Score 28; DE Pred. No. 48; ); Mismatches
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                                                         proteome.
5ED4AC8CE2B336A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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              48;
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                             Length 222;
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                                                                                                                                                                                                                               EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                     Kosugi H.,
                                                                                                                                                                                                                                            a collaboration
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RESULT 6
SPYA_FELCA
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Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                           INIT_MET
                                                                                                                                                                                                                                                                         culties requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGXT OR AGT1.
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Serine--pyruvate aminotransferase, mitochondrial precursor
(EC 2.6.1.51) (SPT) (Alanine--glyoxylate aminotransferase)
(EC 2.6.1.44) (AGT).
AGXT OR AGT1.
                                                                                SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissue-Liver;
MEDLINE-94222101; PubMed-8168541;
Lumb M.J., Purdue P.E., Danpure C.J.;
Lumb M.J., Purdue P.E., Danpure C.J.;
"Molecular evolution of alanine/glyoxylate aminotransferase
"Molecular evolution of alanine/glyoxylate feline gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P41689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPYA_FELCA
                                                    SEQUENCE
                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                       EMBL; X75923; CAA53527.1; -. PIR; S43253; S43253.
                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9685;
                                                                                                                                                              CHAIN
                                                                                                                                                                                                    Transferase;
                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                       Mitochondrion;
                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                            RANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: L-alanine + glyoxylate COFACTOR: Pyridoxal phosphate. SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX ALTERNATIVE PRODUCTS:

Event-Alternative initiation:
                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alanine
                                                                                                                                                                                                                                                                                                                                                                                                      aminotransferases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 AISGSG
                                                                                                                                                                                                                                 PF00266;
                                                                                                                                                                                                                                                                                                                                                                                                                are produced by alternative :
MILARITY: Belongs to class-V
                                                                                                                                                                                                                                                                                                                                                                                                                                            Comment=2 isoforms, Mitochondrial (shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L
                                                                                                                                                                                                                  '00266; aminotran_5; l. PS00595; AA_TRANSFER_CLASS_5;
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                                                                                                                                                                                                                                           IPR000192; Aminotransfv.
                                                      414
100.0%;
ilarity 100.0%;
Conservative (
                                                                                23
231
412
                                                                                                                                  Aminotransferase; Pyridoxal phosphate; Peroxisome; n; Transit peptide; Alternative initiation.

1 23 MITOCHONDRION (BY SIMILARITY).
24 414 SERINE--PYRUVATE AMINOTRANSFERASE,
25 414 SERINE--PYRUVATE AMINOTRANSFERASE,
27 28 414 SERINE--PYRUVATE AMINOTRANSFERASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116
                                                      AA;
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231
414
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                                                      SIMILARITY).
, OD1B01E0E9A199B3
 Score 28; DE Pred. No. 92; ); Mismatches
                                                                               FOR ISOFORM PEROXISOMAL. PYRIDOXAL PHOSPHATE (BY MICROBODY TARGETING SIGN
                                                                                                                       ISOFORM PEROXISOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 initiation;
/ of pyridox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414
                                                                                                                                                                                                                                                                                                                                                                                                                   pyridoxal-phosphate-dependent
                92;
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    pyruvate + glycine.

                                                       CRC64;
                           Length 414;
                                                                                  SIGNAL
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                                                                                              SIMILARITY)
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AISGSG

104

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RESULTA
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DHE4_AC
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Eukaryota; Fungi; 1
Agaricales; Agarica
NCBI_TaxID=5341;
[1]
                                                                                                                                                             P54387;
01-OCT-1996
01-OCT-1996
16-OCT-2001
                                                                                                                    GDHA.
                                                                                                                                01-OCT-1996 (Rel. 34, C)
01-OCT-1996 (Rel. 34, La
01-OCT-2001 (Rel. 40, La
NADP-specific glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFDHDRGNASE.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHE4_LACBI STANDARD; PRT; 450 AA P54388; 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last annotation updat NADP-specific glutamate dehydrogenase (EC 1
                                                                                         Agaricus bisporus
                                                                                                                                                                                                                                                      DHE4_AGABI
                                                                                                                                                                                                                                                                                 AGABI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lorillou S.S., Martin F.F.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ
-!- CATALYTIC ACTIVITY: L-glutamate + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _LACBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006095; GLFV_dehydrog.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
InterPro; IPR000205; NAD_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
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Eukaryota; Fungi; Basidiomyco;
Agaricales; Tricholomataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBUNIT: Homohexamer (By similarity).
-1- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-S238N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                          223 AISGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U31369; AAA82936.1; P24295; 1AUP.
                                                                                                                                                                                                                                                                                                                                                                                                     1 AISGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           450 AA; 48474 MW;
                                           Agaricaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           + NADPH.
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1. 34, Last sequence upda
1. 40, Last annotation ur
1. 40, dest annotation ur
                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                        228
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                                           Basidiomycota; Hymenomycetes; caceae; Agaricus.
                                                                                         (Common mushroom)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Basidiomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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Pred.
                                                                                                                                                                                                                                                      PRT;
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Laccaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B803A30FBAF22090 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
No.
                                                                                                                                                                                update)
                                                                                                                                                                                                                                                      457
                                                                                                                                  update)
(EC 1.4.1.4)
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(EC 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    f databases.
h NADP(+) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                 Homobasidiomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homobasidiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                    (NADP-GDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restrictions
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DHE4_EMENI
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Best Local
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HSSP; P24295; 1AUP.
InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog; 1.
PFAN; PF02812; GLFV_DEHYDROGENASE; 1.
PRINTS; PR00082; GLFU_DEHYDROGENASE; 1.
Oxidoreductase; NADP.
ACT_SITE 111 111
SEQUENCE 457 AA; 49557 MW; 1BF0E97F670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P18819;
01-NOV-1990
01-NOV-1990
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                   nidulans gdhA gene encoding NADP dependent glutamate Mol. Gen. Genet. 218:105-111(1989).
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=89384423; PubMed=2550758;

MENLINE=89384423; PubMed=2550758;

May a sequence and regulation of expression of "Nucleotide sequence and regulation of expression" of the sequence and regulation of expression of expressi
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01-NOV-1990 (Rel. 16, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
NADP-specific glutamate dehydrogenase (EC 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schaap P.J., Mueller Y., Baars J.J.P., Op den Camp H.J.M., Sonnenberg A.S.M., van Griensven L.J.L.D., Visser J.; "Nucleotide sequence and expression of the gene encoding NADP+-dependent glutamate dehydrogenase (gdhA) from Agaricus bisporus."; Mol. Gen. Genet. 250:339-347(1996).
-!- CATALTYIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: Homohexamer (By similarity).
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                                                                                                                                                                                                                    CATALYTIC ACTIVITY: L-glutamate + H(2)O + + NH(3) + NADPH.
SUBUNIT: Homohexamer.
                                                                                                                                                                                 SIMILARITY: BELONGS
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Emericella.
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Pred. No.
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1BF0E97F67078AC4 CRC64;
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HSSP; P24295; 1AUP.
InterPro; IPR006095; GLFV_dehydrog.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF002812; GLFV_dehydrog, 1.
PRINTS; PR00082; GLFV_DEHYDROGENASE;
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr.
Cocle S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy,
Hornsby T., Jagels K., Kregh A., McCean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for centilies requires a license agreement (See http://www.isb-sib.ch or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative amidase amiA2 (EC 3.5.1.4).
AMIA2 OR RY2363 OR MT2432 OR MTCY27.17C.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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ACT_SITE 114 1:
                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Gwinn M.L., Haft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Rolcht A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
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                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                      Bishai W.;
European Bioinformatics Institute. The by non-profit institutions as long
                                                                SWISS-PROT entry is copyright. It is produced through a collaboration entry is copyright. It is produced through a collaboration to the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the swiss in the Swiss Institute of Bioinformatics and the EMBL outstation in the swiss in the
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Mikula A.,
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                                           DOMAIN
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SEQUENCE
                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by another the control of the statement is not removed. Usage by another the control of the statement is not removed. Usage by another the control of the statement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                Bowditch R.D., Baumann P., Yousten A.A.;

"Cloning and sequencing of the gene encoding a 125-kilodalto surface-layer protein from Bacilius sphaericus 2362 and of a cryptic gene.;

J. Bacteriol. 171:4178-4188(1989).

-I- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.

-I- SUBCELLULAR LOCATION: Cell wall.

-I- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1994 (Rel. 30,
01-OCT-1994 (Rel. 30,
01-FEB-1996 (Rel. 33,
Surface-layer 125 kDa
                                                                                                      Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=2362;
MEDLINE=89327128; PubMed=2666389;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus sphaericus.
Bacteria; Firmicutes;
NCBI_TaxID=1421;
                                                                                         CHAIN
                                                                                                                                                           EMBL; M28361; AAA50256.1; PIR; A33856; A33856.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P38537;
                                                                                DOMAIN
                                                                                                                            Pfam; PF00395; SLH; 3.
PROSITE; PS01072; SLH_DOMAIN;
                                                                                                                                        InterPro; IPR001119; SLH. Pfam; PF00395; SLH; 3.
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 Similarity
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 100.0%; llarity 100.0%; Conservative
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Last sequence update)
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protein precursor.
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                                            POTENTIAL.
SURFACE-LAYER 1
SLH 1.
SLH 2.
SLH 3.
SLH 3.
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 Score 28; DE
Pred. No. 2.7
0; Mismatches
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                                                1A9A458EF433788C CRC64;
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                    EMBL; M33557; AAA25975.1; -.
EMBL; AE004476; AAG03782.1; -.
EMBL; M55524; AAA25958.1; -.
PIR; JQ0418; JQ0418.
InterPro; IPR000304; P5CR.
Pfam; PF01089; P5CR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ATCC 15692 / PAO1;
MEDLINB-2043737; Pubmed-10984043;
Stover C.K. Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                 Gene 101:33-44(1991)
                                                                                                                                                                                                                                                                                                                                                             and evidence for a specialised
                                                                                                                                                                                                                                                                                                                                                                                           Whitchurch Mattick J.
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 15692 / PAO1;
MEDLINE=91285432; PubMed=1676385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen."; Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Savioz A., Jeenes D.J., Kocher H.P., Haas D.; "Comparison of proC and other housekeeping genes of Pseudo aeruginosa with their counterparts in Escherichia coli.";
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01-AUG-1991 (Rel. 19, Last sequenc
18-FEB-2003 (Rel. 41, Last annotat
Pyrroline-5-carboxylate reductase
                                                                                                                                                                                                                                                                                                                                                                            "Characterisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene
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STRAIN-90185238; PubMed-2107123;
MEDLINE-90185238; PubMed-2107123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonadaceae;
NCBI_TaxID=287;
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carboxylate + NAD(P)H.
PATHWAY: Proline blosynthesis; third (last) step.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLAT
                                                                                                                                                                                 ween the Swiss Institute of Bioinf
European Bioinformatics Institute
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te reductase (EC 1.5.1
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X
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protein export system widespread i
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1.5.1.2)
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01-NOV-1997
15-JUL-1998
                                                                                               TRANSMEM TRANSMEM
                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                      "Over-expression of a new photo-active halorhodopsin salinarium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    Halobacterium halobium (strain port).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                  TRANSMEM
                                                                                                                                                              PROSITE;
                                                                                                                                                                                 PRINTS; PR00251; BACTRLOPSIN.
                                                                                                                                                                                         Pfam; PF01036; Bac_rhodopsin;
                                                                                                                                                                                                             HSSP;
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                                                                                                                                                                                                                              EMBL; D43766; BAA07823.1;
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                                                                                                                                                                                                                                                         entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                             Biochim.
                                                                                                                                                                                                                                                                                                                                                                                         Otomo J.,
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=96130249; PubMed=8541296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Halorhodopsin
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                                                                                                                                                               PS00950;
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                                                                                                                                                                                                                                                                                                                                                   Biophys. Acta 1240:248-256(1995).
                                                                                                                                                                                                                                                                                              the Swiss Institute of
                                                                                                                                                                                                IPR001425; Bac_rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                         Muramatsu
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276
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(Rel. 35, Last sequence up
(Rel. 36, Last annotation
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                                                                                                                                                    Photoreceptor;
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HELIX B (POTENTIAL).
HELIX C (POTENTIAL).
HELIX D (POTENTIAL).
HELIX E (POTENTIAL).
HELIX F (POTENTIAL).
Score 27;
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PA6725;
01-NOV-1995 (Rel. 32, Created)
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28-FEB-2003 (Rel. 41, Last annotatic
Pyrroline-5-carboxylate reductase (FPROC_OR_ML2430 OR_B2168_C2_211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWI
between
                                                                                                                                                                                                                   InterPro; IPR000304; p5CR.
pfam; pF01089; p5CR; 1.
TIGRFAMS; TIGR00112; proC; 1.
pROSITE; p500521; p5CR; 1.
Oxidoreductase; proline blosy
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Bacteria; Actinobacteria;
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Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.";
Submitted (APR-2001) to the
-i- CATALYTIC ACTIVITY: L-pr
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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg

Belcher R., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FDB-2003 (Rel. 41, Last annotation updat
Pyrroline-5-carboxylate reductase (EC 1.5.)
PROC OR RV0500 OR MT0520 OR MTCY20G9.26.
                                                                                                                                                                            TubercuList; Rv0500;
InterPro; IPR000304;
Pfam; PF01089; P5CR;
                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome sequence. Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterineae; Mycobacteriaceae; NCBI_TaxID=1773;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole genome comparison
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PATHWAY: Proline biosynthesis; third (last) step.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE
                                                                                                                                                                                                                                       ; AE006952; AAK, G70745; G70745;
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Search completed: August 20, 2003, 12:34:52 Job time: 4.38822 secs

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Q8PUG7
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Q9N8A7
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Q8xv21 ralstonia s
Q8xv21 ralstonia s
Q8nqh7 corynebacte
Q971j2 clostridium
Q93tv0 pseudomonas
Q94129 aspergillus
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0976j2 sulfolobus
08zx34 pyrobaculum
0980x4 sulfolobus
0980x7 cryptospori
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Q8pug7 methanosarc
Q27589 methanobact
           pseudomonas
sapergillus
drosophila
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## ALIGNMENTS

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RESULT 1
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STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed-11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).

EMBL; AE007554; AAK78377.1; -.

InterPro; IPR001347; SIS.

Pfam; PF01380; SIS; 1.
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Bacteria; Firmicutes; Clostridia;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
predicted sugar phosphate aminotransferase involved
                                                                                                                                                                                                                                                                          Transferase; Aminotransferase; SEQUENCE 182 AA; 19724 MW;
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EMBL; AP000981; BAB65155.1; -.
InterPro; IPR001347; SIS.
Pfam; PF01380; SIS; 1.
Hypothetical protein; Complete protestical protein; ABAD:
                                                                                                                                                                                                                    "Genome sequence of the aerophilum.";
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01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
Conserved protein with sugar
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                                                                                                                                                                                                    Proc.
                                                                                                                                                                                                                                                                                                                                                                                                   Thermoproteaceae; NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Crenarchaeota; Thermoprotei;
Thermoproteaceae; Pyrobaculum.
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PubMed=11572479;
                                                                                                                                                                                 EMBL;
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SEQUENCE FROM N.A.

STRAIN-ATCC 35092 / DSM 1617 / P2;

STRAIN-ATCC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed-11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

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"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
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01-OCT-2000
01-OCT-2002
                                                                                                                             Chung P.A., Johnson J., Khramtsov N.V., Upton S.J.;
"Cloning and molecular characterization of a gene encoding Cryptosporidium parvum putative 20S proteasome betal-type: DNA Seq. 11:309-314(2000).
                                                                                                                                                                                                                                    MEDLINE=20541292; PubMed=11092745;
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D-arabino 3-hexulose 6-phosphate formaldehyde lyase
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RX MEDLINE-21929760; PubMed-11932238;

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Pealisen I.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Pritchett M.W., Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic

RT and physiological diversity.";

RM InterPro; IPR001347; SIS.

DR EMBL; ABC010808; AAM04800.1; -.

DR InterPro; IPR001347; SIS.

RW Isomerse. Commerce.
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PRINTS; PR00141; PROTEASOME.
PROSITE; PS00854; PROTEASOME_B; 1.
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Archaea; Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina.
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SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTIC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE (BESTERVINE)
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AISGSG 110
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Pred. No.
                                                                                                  Score 28; DB 17;
Pred. No. 3.6e+02;
; Mismatches 0;
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                                                                                                                                                                                                         1237FBA5E824FEC3 CRC64;
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3.5e+02;
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RESULT 7

Query Match

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X MEDILINE-98037514; PubMed-9371463;
A Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Olu D.,
A Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
A Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
A Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
T Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
R EMBL; AE000915; AAB86020.1; ...
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Best Local
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SEQUENCE FROM N.A.
STRAIN-GOE1 / GO1 / ATCC BAA-199 / DSM 3647 /
STRAIN-GOE1 / GO1 / ATCC BAA-199 / DSM 3647 /
MPDITINE-22120827; PubMed-12125824; Merkl)
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isomerase;
SEQUENCE
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01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A., Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C., Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus Fritz H.-J., Gottschalk G.; "The genome of Methanosarcina mazel: evidence for lateral gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanococci; Methanosarcinaceae; Methanosarcina.
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                                                                                                                                                                                                                                                                                                                  Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria;
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                            Pfam; PF01380; SIS;
                                                                                                                                                                                                                                             STRAIN-Delta
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                                                                                                                                                                                                                                                                                      NCBI_TaxID-187420;
                                                                                                                                                                                                                                                                                                      Methanobacteriaceae;
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219 AA; 24122 MW;
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 28218 MW;
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Pred. No.
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 3671BD3FF8D674A8 CRC64;
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01-OCT-2000
01-MAR-2003
                                         MEDLINE-21681879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Mature 415:497-502(2002).
EMBL; AL646071; CAD16391.1; -.
InterPro; IPR000304; PSCR.
Pfam; PF01089; P5CR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical 30.5 kDa profes
CHR1.424.
        TIGREAMS; TIGRO0112; proC; 1.
PROSITE; PS00521; P5CR; 1.
Oxidoreductase; Complete prot
 SEQUENCE
                                                                                                                                                                                                                                                            Q8XVZ1;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable oxidoreductase pyrroline-5-carboxylate red
peptide protein (EC 1.5.1.2)
PROC OR RSC2684 OR RS00037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hall N., Bowman S., Quail M., Ivens A.C., Kay Lennard N.J., Clark L.N., Harris B.R., Melvill Gerrard C., Rajandream M.A., Barrell B.G.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ EMBL; AL929607; CAB95638.1;
                                                                                                                                                                                                                                         Ralstonia solanacearum (Ps
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical SEQUENCE 2:
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Eukaryota; Euglenoz
                                                                                                                                                                                   STRAIN=GMI1000;
                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                Ralstoniaceae;
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271 AA; 3(
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                                                                                                                                                                                                                                        (Pseudomonas solanacearum).
ia; Betaproteobacteria; Burkholderiales;
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                                                                 Tatusov R.L., Sabathe F., Doucette-Stamm I Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis bacterium Clostridium acerobutylicum."; J. Bacteriol. 183:4823-4838(2001). EMBL, AE007572; AAK78547.1; "EMBL, AE007572; AE0075
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed-11466286;
Noelling J., Breton G., Omelchenko M.V., Makar Gibson R., Lee H.M., Dubois J., Qiu D., Hitti
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[nterPro;

IPR000534; Semialdh\_dh

Semialdhyde\_dh;

PF01118;

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RESULT 13
093TVO
1D 093TV
AC 093TV
DT 01-DI
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RESULT
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094199;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Pseudomonas putida glutamate dehydrogenase (gd Submitted (MAY-2001) to the EMBL/GenBank/DDBJ d. EMBL; AF321093; AAK49517.2; -. HSSP; P96110; 1B26. InterPro. Transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02774; Semialdhyde_dhC; complete proteome. seQUENCE 359 AA; 40383 MW: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q93TVO;
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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O1-DEC-2001 (TrEMBLrel.
O1-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                       GDHA.
Aspergillus awamori.
Aspergillus awamori.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Asperg
NCBI_TaxID=105351;
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InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF002812; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFDHDRGNASE.
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STRAIN-PML1;
Syn C.K.C., Magnuson
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   "Characterization and nitrogen source regulation transcriptional level of the gdhA gene of Aspegi'
                                                                   Cardoza R.E., Moralejo Martin J.F.;
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      094129
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                                                                                                                                      STRAIN-ATCC
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Similarity 100.0%;
6; Conservative 0
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                                                                                                    F.J., Gutlerrez

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RESULT 15
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                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN-Tucson 15010-1001.10;

MEDLINE-22426072; PubMed-12537575;

MEDRINE-22426072; PubMed-12537575;

Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoskins Gnirke A., Mungall C.J., Wang A.M., Kronmiller B., Pacl Stapleton M., Wan K., George R.A., de Jong P.J., Botas Celniker S.E.;
                                                                                                                                                                                                                                                 Drosophila littoralis.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=47316;
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Q8I192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006095; GLFV_dehydrog.c. InterPro; IPR006096; GLFV_dehydrog_C. InterPro; IPR006097; GLFV_dehydrog_N, pfam; pF00208; GLFV_dehydrog; 1. pfam; pF02812; GLFV_dehydrog, N; 1.
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HSSP; P24295; 1AUP.
                                                                                            "Assessing the impact of comparative genomic sequence functional annotation of the Drosophila genome."; Genome Biol. 3:RESEARCH0086.1-RESEARCH0086.2002).
EMBL; AX190955; AAO01080.1; .
SEQUENCE 379 AA; 42266 MW; 07B6AE9C97AE5EC6 CRC64;
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Pred. No.
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Pred. No. 6.7
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6.5e+02;
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6.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_phage:*
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Q96QP2
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                                   Q96qp2 homo sapien
Q96qp3 xylella fas
Q3184 caenorhabdi
Q3303 caenorhabdi
Q3306 caenorhabdi
Q17647 caenorhabdi
O17647 caenorhabdi
O62956 picea abies
Q76284 human immun
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Q76286 human immun
Q76287 xanthomonas
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 Q8ejj4 shewanella
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## ALIGNMENTS

RESULT 1

Q9TR48

Q9TR48

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Q9Tr48; 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,

Last sequence update)
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RESULT
Q96QP2
ID Q9
AC Q9
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DT 01
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Q96QP2;
Q96QP2;
01-DEC-2001
01-DEC-2001
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Bos taurus (Bovine).

Bus taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;

Bovidae; Bovinae; Bos.

MCBI_TaxID=9913;
                                                                                                                                                                                                                   HOri O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X., Nagashima M., Lundh E.R., Vijay S., Nitecki D.;
Nagashima M., Lundh E.R., Vijay S., Nitecki D.;
"The receptor for advanced glycation end products (RAGE) is a cellular binding site for amphoterin. Mediation of neurite outgrowth and co-expression of rage and amphoterin in the developing nervous system.";
J. Biol. Chem. 270:25752-25761(1995).
SEQUENCE 10 AA; 1050 MW; 23B89A286761EB18 CRC64;
                                                                                                                                                                                                                                                                                                                  MEDLINE-96029671; PubMed-7592757;
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RA Simpson A.J.G., Reimach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.,
RA Colauto M.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Meto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Lemos M.F., Lopes S.A., Lopes S.L., Gruber A.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Manda C.F.M., Miracca E.C., Niyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Manda A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Menok C.F.M., Morber G.G., Santelli R.V., Sawasaki H.E.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA de Souza A.P., Terenzi M.F., Verjovski-Almeida S., Vettore A.L.,
RA de Souza A.P., Terenzi M.F., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
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01-CCT-2000 (TrEMBLrel. 1:
01-MAR-2002 (TrEMBLrel. 1:
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hube F., Reverdiau-Moalic P., Iochmann "Characterization of the human tissue (TFPI-2) gene promoter region."; Submitted (JUL-2001) to the EMBL/GenBa EMBL; AY044097; AAK72693.1; -. NON_TER 14
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in; Complete proteome.
3348 MW; 51A14263E99F91A3 CRC64;
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Primates;
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WormPep;
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01-NOV-1996
01-MAR-2003
        Submitted (NOV-1996) to the EMBL; 278067; CAB01526.1; -EMBL; 29849; CAB07428.1; -Wormbep; H12D21.1; CE15223. Wormbep; ZC412.7; CE15223.
                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                 Mcmurray
                                                           SEQUENCE FROM N.A.
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ZC412.7 OR H12D21.1.
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                                                                                                              NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                             WormPep; W06A7.5; SEQUENCE 34 AA;
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Science 282:2012-2018(1998).
EMBL; 278066; CAB01519.1; -.
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Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caen
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MEDLINE=99069613; PubMed=9851916;
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01-NOV-1996 (TrEMBLrel.
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C40H5.1 PROTECTION.
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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"Genome sequence of the nematode investigating biology."; Science 282:2012-2018(1998). EMBL; Z81482; CAB03952.1; -. WormPep; C40H5.1; CE08649.
                                                                                                                                                                                                                                                                                                            investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z78067; CAB01529.1; -.
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Kluemper S., Kanka S., Riesner D., Etscheid M.;

"Characterisation of a Norway spruce chloroplast DN
nucleotide sequences of rp123, rp12, rps19, rp122,
pseudo-ndhC and a residual inverted repeat B.";
pseudo-ndhC (MAR-1997) to the EMBL/GenBank/DDBJ datab
EMBL; U92462; AAC95502.1;
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NCBI_TaxID=3329;
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                mutations in the V3 region of the J. Virol. 68:6130-6135(1994). EMBL; D34603; BAA07002.1; -. InterPro; IPR000777; GP120.
                                                                                        Shimizu N.S., Shimizu N.G., Takeuchi Y., "Isolation and characterization of human variants Onfectious to brain-derived cell
                                                                                                                              SEQUENCE FROM N.A.
STRAIN-HIV-I[GUN-4];
MEDLINE-94335139; PubMed-7980782;
Shimizu N.S., Shimizu N.G., Takeu
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NCBI_TaxID=11676;
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                         SEQUENCE FROM N.A. STRAIN-HIV-1[GUN-4]; Shimizu N.S.;
                                                                                                           Viruses; Retroid viruses; NCBI_TaxID=11676;
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"Isolation and characterization of human immunodeficiency virus variants Onfectious to brain-derived cells: detection of common mutations in the V3 region of the env gene of the variants.";
J. Virol. 68:6130-6135(1994).
EMBL; D34602; BAA07001.1;
"The common structure of the variants."
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MEDLINE-94335139; Pu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=HIV-1[GUN-4];
Shimizu N.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; Retroid
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.

Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q76283;
01-NOV-1996
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4; Conser
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6 (TrEMBLrel. 01,
2 (TrEMBLrel. 22,
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                                                                                                                                Retroviridae; Lentivirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A3670DE7AF40F415 CRC64;
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7.9e+02;
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Q8KAT7
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Best Local S
Matches 4
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C STRAIN-TLS / ATCC 49652 / DSM 12025;

X MEDLINE-22103685; PubMed-12093901;

X MEDLINE-22103685; PubMed-12093901;

X Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

A Lisen J.A., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

A Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

A Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

A Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

A Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

A Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

"The complete genome sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium.";

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
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Best Local :
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P74973;
O1-FEB-1997
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01-OCT-2002
01-OCT-2002
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J. Virol. 68:6130-6135(1994).
EMBL; D34601; BAAD7000.1;
InterPro: IPBRAG7777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE012956; AAM73285.1; TIGR; CT2068; -.
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MEDLINE=94335139; Pu
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37 AA; 4349 MW; 545A837202D7F219 CRC64;
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SEQUENCE
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EMBL; U51094; AAB94635.1; -.
HSSP; Q01745; 1GOF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-DSM 4527;
Niessen M.L., Vogel R.F.;
"Specific identification of Fusarium graminearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Galactose oxidase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gibberella zeae (Fusarium graminearum).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocrealas; Nectriaceae; Gibberella.
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002048; EF-hand.
InterPro; IPR000421; FA58_C.
PROSITE; PS00018; EF_HAND; 1.
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InterPro; IPR005467; His_kinase.
Pfam; PF02518; HATPase_c; 1.
PROSITE; PS50109; HIS_KIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A two-component signal tranduction system of Xanthomonas pv. phaseoli var. fuscans strain BXPF65."; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U69111; AAB09063.1; -.
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Xanthomonas campestris.

Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

Xanthomonadaceae; Xanthomonas.
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Chan J.W.Y.F., Maynard S.,
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    PRELIMINARY;
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Mismatches
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EMBL; X54015; CAA37962.1; -.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
InterPro; IPR00567; His_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q04528;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Genes for sensor and regulator protein (Fragment).
                                                                                                                                                                                                                                                         STRAIN-pathovar: campestris;
MEDLING-91042416; PubMed-2233675;
Osbourn A.E., Clarke B.R., Stevens B.J.H., Daniels M.J.;
"Use of oligonuclectide probes to identify members of two-component systems in Xanthomonas campestris pathovar campestris.";
MOI. Gen. Genet. 222:145-151(1990).
-i- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
                                                                                                            SEQUENCE
                                                                                                                         Kinase; Phosphorylation; Sensory transduction; Transferase
                                                                                                                                                 PROSITE; PS50109; HIS_KIN; 1.
                                                                                                                                                                              Pfam; PF02518; HATPase_c;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=339;
                          1 GLSI 4
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GLSI 12
                                                                                                       46 AA; 4824 MW; 1A3C266837B0F6C5 CRC64;
                                                     Conservative
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## ALIGNMENTS

RESULT 1 AAU98275

AAU98275;

15-AUG-2002 (first entry)

AAU98275 standard; peptide; 8

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Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ag85; epitope; vaccine; tuberculosis; mycolyltransferase; HLA-A*02001; Mycobacterium tuberculosis; Mycobacterium leprae; Mycobacterium bovis; Mycobacterium ulcerans; Mycobacterium avium; antibacterial; Mycobacterium avium; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. tuberculosis Ag85 derived immunodominant T cell epitope #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
    30-NOV-2000; 2000EP-0204268
                                                                                              30-NOV-2000; 2000EP-0204268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                            05-JUN-2002
                                                                                                                                                                                                                                                                                     EP1211260-A1
                                                                                                                                                                                                                                                                                                                                                                                    /note- "Amino acid contributing to the HLA-A*02001 binding motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Amino acid contributing
binding motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the HLA-A*02001
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Saccharomyces cer Bovine glial cell Saccharomyces Saccharomyces

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RESULT 2
AAR51217
ID AAR5
XX AAR5
AC AAR5
XX DT 25-M
DT 25-M
DT 02-M
XX Brad
KW Brad
KW Trea
XX Synt
XX Synt
XX Wodi
FT Modi
FT Misc
FT Misc
FT W094
XX W094
XX W994
XX W994
XX W896-6
XX W896-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
               08-SEP-1993;
                                                                               WO9406453-A1
                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to peptide (PI) derived from an Ag85 protein of mycobacterium (which is associated with mycolyltransferase activity and is involved in cell wall synthesis), comprising 8-11 amino acids, and capable of inducing proliferation of MIC class I-restricted CD8+ T cells in vivo. Also included are (1) a peptide comprising PI flanked by amino acids representing antigen processing sites; (2) a polypeptide comprising at least two of the peptides in (1); (3) a nucleic acid encoding one of the claimed peptides or polypeptides; (4) a vector comprising the above nucleic acid; (5) a host cell comprising the above nucleic acid; (5) a host cell comprising the above nucleic acid; (5) a detecting and/or enumerating CD8+ T cells against mycobacterium, comprising tetrameric complexes of MIC (major histocompatibility group) class I and one of the claimed peptides or polypeptides. The molecules of the invention are used to prepare a
                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                  Bradykinin
                                                                                                                                                                                                                                                                                                            A generic Bradykinin antagonist peptide.
                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
02-NOV-1994
                                                                                                                                                                                                                                                                Treatment
                                                                                                                                                                                                                                                                                                                                                                                                  AAR51217;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAR51217 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine against mycobacterium (e.g. Mycobacterium tuberculosis, Mycobacterium leprae, Mycobacterium bovis, Mycobacterium ulcerans, Mycobacterium avium) and thus protect against diseases such as tuberculosis. The present sequence is an M. tuberculosis Ag85 derived immunogenic peptide of the invention binding to HLA-A*0200 (human laukhourt against feet against to HLA-A*0200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide of 8-11 amino acids derived from the Ag85 protein of mycobacterium induce proliferation of MHC class I-restricted CD8+ _{\rm T} cells and are useful to vaccinate against infection by mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (human leukocyte antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 6; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZIEK-) ACAD ZIEKENHUIS LEIDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GLSI 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                             n antagonist peptide; of inflammatory react
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΑĄ;
                                                                                                                                                                                                                                                                                                                                             (updated)
(first entry)
             93WO-US08220
                                                                                                                                /note=
                                                                                                                                                                                  Location/Qualifiers
                                                                                                               'note=
                                                                                                                                                               'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                             "D-form residue
                                                                                                                                                                                                                                                        tide; 5-position; non-aromatic residue reactions; reduce pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 23;
9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA-A*02003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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RESULT 3
AAR82116
ID AAR8
XX
AC AAR8
AC AAR8
DT 25-M
XX
XX
MEla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                            Melanoma-specific immunogen pMel.17 - are highly potent adoptive immuno-therapy
                                                                                                                                                                                                                                                                                            Melanoma; cytotoxic
                                                                                                         WPI; 1995-302688/39
                                                                                                                             Cox AL,
                                                                                                                                                                        29-APR-1994;
16-FEB-1994;
                                                                                                                                                                                                        16-FEB-1995;
                                                                                                                                                                                                                                                   W09522561-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR51217 is an example of a generic bradykinin antagonist peptide having a non-aromatic residue in the 5-position. The antagonist peptide inhibits the bradykinin reponse when injected as a bolus admixture of bradykinin plus antagonist by either the ia. or iv. route of administration, or when administered as an infusion. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                   (UYVI-)
                                                                                                                                                                                                                             24-AUG-1995
                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                        Melanoma-specific mutant immunogen epitope 9mer peptide
                                                                                                                                                                                                                                                                                                                                                  25-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                       AAR82116;
                                                                                                                                                                                                                                                                                                                                                                                           AAR82116 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antagonistic bradykinin analogues with non-aromatic amino acid in the 5-position - are useful for treating inflammatory reactions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gera L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 44; Page 19; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-118152/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypotension, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GERA/) GERA L.
(SRIV/) SRIVASTAVA V.
(STEW/) STEWART J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                   UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GLSI 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conserv
                                                                                                                             Engelhard VH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Srivastava V,
                                                                                                                                                                                                                                                                                          immunogen; epitope; homologue; vaccine; immunotherapy;
T cell; lymphocyte; HLA-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nilarity (100.0%)
Conservative 0
                                                                                                                                                  VIRGINIA PATENT FOUND
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                      94US-0234784.
94US-0197399.
                                                                                                                                                                                                        95WO-US01991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-0942317
                                                                                                                                                                                                                                                                                                                                                                                          peptide;
                                                                                                                             Hunt DF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pages; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stewart
                                                                      comprises epitope(s) homologous with stimulators of HLA-A2+CTL's useful in
                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 15;
Pred. No. 9.3e+05;
; Mismatches 0;
                                                                                                                            Shabanowitz
                                                                                                                            ľ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                            Slingluff CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0,

A melanoma-specific immunogen homologous with pMel-17 comprises or more CTL (cytotoxic T lymphocyte) epitopes from the group AAI AAR82194 capable of eliciting a CTL response. The epitopes AAR8.

Example

8; Page 51; 148pp; English.

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AAR5121
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR82108 are of particular interest. The immunogen can be used for partial protection in mammals against melanoma peptides which are homologous with pMel-17 are highly potent stimulators of HLA-A2+CTLs in several cell lines and can be used in immunotherapy or incorporated into immunogenic conjugates as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A generic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR51218;
                     AAR51217 is an example of a generic bradykinin antagonist peptide having a non-arcmatic residue in the 5-position. The antagonist peptide inhibits the bradykinin reponse when injected as a bolus admixture of bradykinin plus antagonist by either the ia. or iv. route of administration, or when administered as an infusion. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                               31-MAR-1994
                                                                                                                                                                                                                                                                                                                                     W09406453-A1
                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bradykinin antagonist peptide; 5-position; non-aromatic residue Treatment of inflammatory reactions; reduce pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR51218 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                        08-SEP-1993;
                                                                                                                                     Antagonistic bradykinin analogues with non-aromatic amino acid in the 5-position - are useful for treating inflammatory reactions,
                                                                                                                                                                                               Gera L,
                                                                                                                                                                                                                   (GERA/) GERA L.
(SRIV/) SRIVASTAVA V.
(STEW/) STEWART J M.
                                                                                                                                                                                                                                                                   11-SEP-1992;
                                                                                                     Example 45; Page 19;
                                                                                                                          hypotension,
                                                                                                                                                                         1994-118152/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ب
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLSI 4
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                                                                                                                                                                                               Srivastava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bradykinin antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                             etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                                                                                                                                                                                                                                   92US-0942317
                                                                                                                                                                                                                                                                                        93WO-US08220
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                 /note-
                                                                                                                                                                                                                                                                                                                                                                                             label-
                                                                                                                                                                                                                                                                                                                                                                                                                  'note" "D-form residue"
                                                                                                                                                                                               <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                      29 Pages; English.
                                                                                                                                                                                                                                                                                                                                                                                             4Hyp
                                                                                                                                                                                               Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB
Pred. No. 9.3
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16;
. 9.3e+05;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Sequence

10

Saccharomyces

cerevisiae;

complementary peptide; peptide

identification;

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RESULT 6
AAG86718
ID AAG8
XX
AC AAG8
XX
DT 11-S
XX
DE Sacc
XX
XX
Sacc
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                                                                                                                             밁
                                                                                                                                                                  Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                         The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
                                                                                                                                                                                                                                                                                                                 A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200142277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG95974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG95974 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                           13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-408419/43
                                                                                                                                                                                                                                                                                                                                                                                   Roberts GW,
                                                                             AAG86718 standard;
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                Example 4; Page 353; 646pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEOM LTD.
                    Saccharomyces
                                       11-SEP-2001
                                                         AAG86718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complementary peptide; ligand; drug discovery; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GLSI 4
                                                                                                                             σ
                                                                                                                                                1 GLSI 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                   4
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                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLSI 8
                                                                                                                             GLSI
                                                                                                                                                                                                          10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-GB04776
                                       (first entry)
                    cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                           99GB-0029464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide;
                                                                              Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                             100.0%;
                     peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                               10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18;
Pred. No.
                                                                                                                                                                             Score 18; DB 22;
Pred. No. 1.2e+02;
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                                                                                                                                                                     Mismatches
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                     SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>8</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15;
                      ŏ:
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                      1667.
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                                                                                                                                                                                      Length 10;
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                                                                                                                                                                     Gaps
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RESULT 7
AAG86810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
Identifying complementary peptides by
                                                   WPI; 2001-367863/38.
                                                                                           Roberts
                                                                                                                                                                              13-DEC-1999;
                                                                                                                                                                                                                         13-DEC-2000;
                                                                                                                                                                                                                                                                   14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae; complementary peptide; peptide identification;
                                                                                                                                                                                                                                                                                                            WO200142276-A1
                                                                                                                                                                                                                                                                                                                                                    Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                 drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG86810;
                                                                                                                                    (PROT-) PROTEOM LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded in the eukaryote genome. The peptides may be used as and drugs for drug discovery and as lead ligands for drug desdevelopment. The present sequence is a complementary peptide carcharymeros corrected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoded in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by analysis of protein and nucleotide sequence databases from eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target pure complementary peptides interact with their relevant target pure process of the complementary peptides interact with their relevant target pure process of the complementary peptides interact with their relevant target pure process of the complementary peptides in the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the identification of complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 260; 488pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying complementary peptides by nucleotide sequence databases, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roberts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug discovery; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analysis of protein and
                                                                                                                                                                                                                                                                                                                                                                                                 discovery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-367863/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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                                                                                           GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEOM LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLSI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLSI 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                         Heal JR;
                                                                                                                                                                                                                         2000WO-GB04773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerevisiae peptide, SEQ ID NO: 1759.
                                                                                                                                                                                                                                                                                                                                                    cerevisiae.
                                                                                                                                                                              99GB-0029471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                          design
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
    analysis of protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analysis of protein in drug design -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cary peptides from higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        design and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as reagents
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 Query Match
Best Local Similarity
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Best Local Similarity
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                                                                         The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
                                         Sequence
                                                                   Saccharomyces cerevisiae
                                                                                                                                                                                    Example 3; Page 272; 488pp; English.
                                                                                                                                                                                                              nucleotide
                                                                                                                                                                                                                                                                               Roberts GW,
                                                                                                                                                                                                                         Identifying complementary peptides by
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae; complementary peptide; peptide identification; drug discovery; drug design.
                                                                                                                                                                                                                                                                                                        (PROT-) PROTEOM LTD.
                                                                                                                                                                                                                                                                                                                                  13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                           13-DEC-2000; 2000WO-GB04773
                                                                                                                                                                                                                                                                                                                                                                                     14-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG86812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG86812 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces
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development. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoded in the eukaryote genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleotide sequence databases, useful in drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 272; 488pp; English.
                                                                                                                                                                                                                                                     2001-367863/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GLSI 4
||||
4 GLSI 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                       10
                                                                                                                                                                                                              sequence databases, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                             Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                       A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e eukaryote genome. The peptides may be used as drug discovery and as lead ligands for drug des
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerevisiae.
                                                                                                                                                                                                                                                                                                                                  99GB-0029471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence is a complementary
 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
 Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:
                                                                                                                                                                                                           analysis of protein in drug design -
DB 22;
. 1.2e+02;
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            Length
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design and
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Matches

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RRESULT 9
AAR6712
ID AAR68
XX AAR66
XX DT 25-N
XX G11i
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RESULT 10
AAR86638
ID AAR86
XX
AC AAR86
XX
DT 03-JU
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
"~+~hes 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating GGF2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glial cell growth factor-1; GGF-1; mammalian muscle cell treatment; skeletal; cardiac; smooth; acetylcholine receptor deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR67162 standard; peptide;
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02-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1993;
08-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09426298-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine glial
                                                                                                                                                                                                                                                                                                                                                                         AAR67153-R67163 and AAR67174-R67183 are bovine glial cell growth factor-1 (GGF-1) peptide fragments. A 30-36kD polypeptide factor known to have glial cell mitogenic activity, which includes one of the above peptide fragments in its amino acid sequence is claimed. The polypeptide can be used to treat a variety of mammalian skeletal, cardiac and smooth muscle diseases, including acetylcholine receptor deficiency.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Page 90; 241pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-006353/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gwynne DI, Marchionni M, Sklar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CAMB-) CAMBRIDGE NEUROSCIENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor.
  03-JUL-1996
                                       AAR86638;
                                                                                AAR86638 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          w
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                                                                                                                                                                             GLSI 4
GLSI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mammalian muscle diseases and disorders - by admin. of other specified polypeptide(s) which bind the p185erbB2
                                                                                                                                                                                                                                                                                                                                        14 AA;
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell growth factor-1 (GGF-1) peptide fragment.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
  (first entry)
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94US-0209204.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Lys, Arg"
                                                                              peptide; 14
                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                         Score 18; DB 16;
Pred. No. 1.8e+02;
Mismatches 0;
                                                                                  B
                                                                                                                                                                                                                                                                                                   Length 14;
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                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                  0;
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AAR49865
ID AAR49865
XX
ARAGEMENT ARAGEMENT ARAGEMENT 25-MJ
DT 12-SI
DT 12-SI
DT 12-SI
CGGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR86629-R86657 represent fragments of bovine glial growth factor I
(GGF-I). These fragments were obtained by Jysyl endopeptidase and
protease v8 digests. These sequences have Schwann cell mitogenic
activity in the presence of foetal calf plasma. These sequences (and
human GGF2, see AAR86628) are used to stimulate mitogenesis of glial
cells, for prophylaxis or treatment of a pathophysiological condition of
the nervous system in a mammal. Also, for identification of a receptor,
for treatment of conditions of peripheral nerve damage (e.g.
centreatment of conditions of peripheral nerve damage (e.g.
centreatment of conditions of Schwann cells), treatment of
neurodegenerative disorders in mammals, for inducing neural
centreated by inhibiting this sequence binding to its receptor.
These peptides are also able to induce synthesis of acetylcholine
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glial growth factor; GGF; human; hGGF2; Schwann cell; mitogenesis; GGF-I; glial cell; therapy; peripheral nerve damage; demyelination; bowlne; glial tumour; fibroblast proliferation; wound repair; multiple sclerosis; neurodegenerative disorder; neural regeneration; acetylcholine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGF I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen MS, Goodearl AD, Stroobant P, Waterfiel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glial growth factors with Schwann prophylaxis or treatment of nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-030329/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CAMB-) CAMBRIDGE NEUROSCIENCE. (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 9; 199pp;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                     AAR49865 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sclerosis
          Sequence of (GGF III).
                                                                    25-MAR-2003
12-SEP-1994
                                                                                                                             AAR49865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tryptic peptide GGF-I 10.
                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                         1 GLSI 4
                                                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                    GLSI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                             14 AA;
                                                                                                                                                                                                                                                                                                                                                  Conservative
                            tryptic digest peptide of bovine glial growth factor III
                                                                    (updated)
(first end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterfield M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9405-0249322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US06846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Lys, Arg
                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 17;
Pred. No. 1.8e+02;
                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell mitogenic activity - for disorders, e.g. Multiple Sclerosis
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Gaps

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Length 14;

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Minghetti

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RESULT 12
AAW18171
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Best Local S
Matches 4
06-DEC-1995;
23-MAY-1995;
20-OCT-1995;
31-OCT-1995;
                                                           23-MAY-1996;
                                                                                                           W09637219-A1
                                                                                                                                                          Vaccine; vaccinating agent; M.tuberculosis; virus; fungus; protozoan; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                              A novel polypeptide was purified from bovine pituitaries. It has mitogenic activity stimulating the division of Schwann cells, and exhibits a mol. wt. of 43-35kD when carrying native glycosylation. It was digested with trypsin and lwylendopeptidase to obtain novel peptides AAR49858-R49866 and AAR49867-R49871 respectively. When peptides AAR49866-R49866 were sequenced to completion it was found that none of these sequences is apparently related to GGF-I or GGF-II peptide sequences. A polypeptide contg. any of the sequences in AAR49858-AAR49871 is claimed, as is DNA encoding each of the peptides. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                    28-NOV-1996
                                                                                                                                    Mycobacterium
                                                                                                                                                                                                Immunodominant
                                                                                                                                                                                                                                                AAW18171;
                                                                                                                                                                                                                                                                     AAW18171 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 32; Page 31; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide factor and peptide(s) from bovine pituitary having mitogenic activity in stimulating division of Schwann cells, used for therapy, prophylaxis, diagnosis of neuro-degenerative disease, glial cell tumours, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glial growth factor; GGF III; mitogen; Schwann cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodearl ADJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                   GLSI 10
                                                                                                                                                                                                                                                                                                                                                          GLSI 4
                                                                                                                                                                                                                                                                                                                                                                                                                                15 AA;
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                    (first entry)
95US-0568357.
95US-0447398.
95US-0545926.
95US-0551149.
                                                                                                                                                                                          epitope from Mycobacterium tuberculosis 30KD protein.
                                                          96WO-US07781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stroobant P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92GB-0017316
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                                                                                                                                                                                                                                                                                                                                                                                           0.0%;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                     DB 15;
                                                                                                                                                                    pathogen; bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goodearl AD
                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                              Indels
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CC against Mycobacterium pathogens comprises at least one immunodominant epitope of at least one majorly abundant coextracellular protein, i.e. the M.tuberculosis 110, 80, 71, 58, 45, CC 32A, 32B, 30, 24, 23.5, 23, 16, 14 or 12 kD proteins, or their cc analogues, homologues and subunits. The present sequence represents an CC immunodominant epitope from the major abundant extracellular product CC 30 KD protein. The vaccinating agents are used to protect against (or to treat existing) infections by Mycobacterium (especially M. CC tuberculosis) while the epitopes can also be used to detect presence CC of an immune response to a Mycobacterium pathogen. The vectors, CC containing the DNA for the extracellular proteins, are used to transform CC cells for production of recombinant DNA molecules. More generally the DNA from other pathogens can be used in vaccines, e.g. against other CC DNA can be used, a wide range of effective compositions can be produced. CT they generate a response against the antigens most often found on CC infected cells during the infection, regardless of the strength or Specificity of the immune response. The vaccines are easy to produce CC and less toxic than known killed or attenuated vaccines, so can be given to immunocompromised subjects, e.g. those with HIV infection.
Query Match
                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccines derived from M.tuberculosis major abundant extracellular proteins - are easy to prepare and less toxic than conventional killed or attenuated vaccines, useful for protecting against or treating Mycobacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harth G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horwitz MA
                                            15
                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
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Matches
                                 Local
σ
             1 GLSI 4
                          4;
                                Similarity
GLSI
                          Conservative
8
                                100.0%;
                          0;
                         Score 18; DB 18;
Pred. No. 1.9e+02;
; Mismatches 0;
                                      Length 15;
                          Indels
                         0;
                         Gaps
                         0;
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AAW7
             AAW75598
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δÃ.

AAW75598 standard; peptide; 15

M. tuberculosis 30 kD protein 23-OCT-1998 (first entry) derived peptide 12 (residues 56-70).

Synthetic Mycobacterium tuberculosis; vaccination; extracellular product; immunodominant epitope; interleukin-12; MF59; immune response; opsonising humoral response; intracellular pathogen. 21-JAN-1997; 23-JUL-1998. WO9831388-A1 Mycobacterium 15-JAN-1998; 97US-0786533 98WO-US00942

(REGC ) UNIV

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Sequences shown in AAW75587 to AAW75641 represent synthetic peptides cc derived from the native 30kD major secretory protein of M. tuberculosis. Cc These peptides are used for splenic lymphocyte profileration assays to cidentify the immunodominant T-cell epitope of the 30kD protein. The cc invention provides an agent for vaccinating mammals against Cc Mycobacterium. The agent comprises at least one of the major abundant cc extracellular 110, 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or cc 12 kD proteins of M. tuberculosis, or at least of their immunodominant cc epitopes and interleukin-12 (II-12) or MF59 as adjuvants. The agent cc containing the nucleic acid encoding the extracellular products are used ct raise a protective or therapeutic immune response against cc mycobacterium, specifically M. tuberculosis. The immunodominant epitopes and inso be used (typically in a cutaneous hypersensitivity test) to detect an immune response to vaccination. Preparation of the agent does not require selection of the most immunogenic products, so large scale production and purification are easy, resulting in a consistent, cc standardised formulation, having lower toxicity than killed or attenuated component) and are safe even in immunocompromised components and are safe even in immunocompromised component even development of an opsonising humoral response that the consistence of the second intracellular pathogens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccines against Mycobacterium containing major extracellular proteins - used to, e.g. induce protective and therapeutic immune responses, and for detecting an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 28; Page 96; 236pp; English.
                                                                                                                                                                                                                                                               Mycobacterium tuberculosis; vaccination; extracellular product; immunodominant epitope; interleukin-12; MF59; immune response; opsonising humoral response; intracellular pathogen.
                                                                                                                 15-JAN-1998;
                                                                                                                                                                                                                  Synthetic.
Mycobacterium
                                                                                                                                                                                                                                                                                                                                   M. tuberculosis 30 kD protein
                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                  AAW75599
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW75599 standard; peptide; 15
               Harth G,
                                                                                  21-JAN-1997;
                                                                                                                                                                                    W09831388-A
                                               (REGC ) UNIV CALIFORNIA
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                   Horwitz MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ξ
                                                                                                                                                                                                                   tuberculosis
                                                                                  97US-0786533
                                                                                                                   98WO-US00942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB
Pred. No. 1.9
D; Mismatches
                                                                                                                                                                                                                                                                                                                                   derived peptide 13 (residues 61-75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19;
1.9e+02;
nes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 15;
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RESULT 15
AAY65578
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Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 28; Page 96; 236pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-413815/35
                                                                                 23-APR-1998;
09-SEP-1998;
08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                             Oestrogen receptor; estrogen; estradiol; oestrogen response element; ERE; binding; biological activity; fingerprint; molecular braille; cellular braille; modulation; tamoxifen; breast cancer; oestoporosis; selective oestrogen receptor modulator; identification; characterisation; classification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY65578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY65578 standard; Peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oestrogen
                                                                                                                                                                                                                                                       W09954728-A2
                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                      26-MAR-1999;
                                                                                                                                                                                                                 28-OCT-1999
                                        (NOVA-) NOVALON PHARM CORP.
                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spread intracellular pathogens.
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Hamilton PT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                 98US-0082756.
98US-0099656.
99US-0115345.
                                                                                                                                                                         99WO-US06664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERE binding peptide 178-beta.
    Fowlkes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
    DM,
      Buehrer B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19;
.9e+02;
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    Barnett T;
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The present invention describes a method for predicting the biological activity of new receptor modulating compounds (I) using novel oligomeric CC peptides (biokeys) which have differential abilities to bind to 2 CC different receptor conformations. The method is used to identify new CC drugs that are physiological or pharmacological agonists/antagonists and CC conditions. The system may be used as a primary screening tool to CC conditions. The system may be used as a primary screening tool to CC characterise selective oestrogen receptor modulators (SERMs) in terms of CC agonist and antagonist function and to predict possible clinical effects of SERMs such as tissue and receptor specificity. The method can also be CC components are producing agonistic and antagonistic activity. The method CC components are producing agonistic and antagonistic activity. The method CC glucocorticoid, thyroid, vitamin D, beta-adrenergic, dopamine and CC epidermal growth factor, to identify, characterise and classify De used with other receptors (e.g. progesterone, androgen, CC modulators of receptor activity. Peptides comprising a LIXIL motif may be used to modulate the oestrogen receptor in treating e.g. breast and CC ovarian cancer and ameliorating the effects of menopause, including costeoporosis. AAV65439 to AAV65622 represent oestrogen receptor in the exemplification of the present invention. AAZ35740 to AAZ35745 cc invention.
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2.2; Page 162; 219pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methods for identifying new receptor modulators, especially estrogen modulators to treat tamoxifen refractory breast cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McDonnell DP, Christensen DJ;
15 AA;
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Search completed: August 20, 2003, 12:33:42 Job time: 9.79518 secs 밁 δÃ Matches Query Match Best Local Similarity 9 GLSI 12 1 GLSI 4 h 100.0%; Similarity 100.0%; 4; Conservative 0; Score 18; DB 21; Pred. No. 1.9e+02; ; Mismatches 0; Length 15; Indels 0 Gaps

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Sequence 74, Appl Sequence 2048, Appl Sequence 205, Appl Sequence 15, Appl Sequence 15, Appl Sequence 17, Appl Sequence 40950, A Sequence 40950, A Sequence 40950, A Sequence 4129, A Sequence 42129, A Sequence 42129, A Sequence 550, Appl Sequence 550, Appl Sequence 550, Appl Sequence 57, Appl Sequence 119, Appl Sequence 119, Appl Sequence 119, Appl Sequence 119, Appl Sequence 1063, Appl Seque

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Minimum DB seq
Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                              Result
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                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      •
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length: 2000000000
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                   : /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
0: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
1: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/USIOC_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USIOC_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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US-09-300-4258-29

US-09-572-4048-2168

US-10-190-082-599

US-09-953-510-48

US-09-953-510-49

US-10-147-255-48

US-10-147-255-49

US-09-80-748-2174

US-09-80-748-2186

US-09-80-748-2186

US-09-80-748-2186

US-09-80-748-2186

US-09-90-1225-61

US-09-991-225-62

US-09-991-225-63
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                                                                                                                                                                                                                     Description
     Sequence 29, Appl
Sequence 599, App
Sequence 599, App
Sequence 49, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 50, Appl
Sequence 2174, Appl
Sequence 2174, Appl
Sequence 2186, Appl
Sequence 2980, Appl
Sequence 62, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 63, Appl
                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B; OTHER INFORMATION: antibody clone US-09-300-425B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-09-300-4258-29
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                                                                                                                                                                                                                                               TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGIOGENESIS FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION UNMEER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION UNMBER: 09/075,338
PRIOR APPLICATION UNMBER: 09/075,338
PRIOR FILING DATE: 1988-05-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/09300425B publication No. US20030045681A1 GENERAL INFORMATION:
                                                                                                     Matches
                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VITI, Francesca
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                      LENGTH:
                                                                                                                   Local Similarity
                                                                             1 GLSI 4
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15 US-10-225-567a 2048
15 US-09-814-604-26
11 US-09-812-26-12
11 US-09-922-226-12
11 US-09-922-226-165
12 US-09-964-761-41951
12 US-09-91-225-12
12 US-09-991-225-12
12 US-09-991-225-13
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US-09-864-761-48997
US-09-864-761-43280
US-09-864-761-43280
US-09-864-761-43280
US-09-864-761-43280
US-09-861-717-34
US-09-764-800-550
US-09-764-800-557
US-09-864-761-48544
US-09-764-853-439
US-09-764-853-71059
US-09-764-853-726
US-09-764-877-1059
US-09-764-877-1053
US-09-764-877-726
US-09-809-391-575
US-09-809-391-575
US-09-909-391-575
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Pred. No. 4.4
0; Mismatches
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4.4e+05; DB 11;

Length 4 Indels

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CITY: Los Angeles

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US-09-953-510-48
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                                                                            Sequence 48, Application US/09953510
Patent No. US20020131975A1
GENERAL INFORMATION:
APPLICANT: Horwitz, Marcus A.
TITLE OF INVENTION: Abundant Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-10-190-082-599
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LENGTH: 12
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Publication:
GENERAL INFORMATION:
APPLICANT: Lasky, Lawrence A.
APPLICANT: Sidhu, Sachdev S.
                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-572-404B-2168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/303,634 PRIOR FILING DATE: 2001-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/190,082 CURRENT FILING DATE: 2002-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sidhu, Sachdev S.
APPLICANT: Held, Helke A.
TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2168, Application US/09572404B Publication No. US20030078374A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: sequence located in PMEL17 OR D12S53E at 164-173 and may interact OTHER INFORMATION: Sequence 2167 in this patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                Local Similarity 100.0%; es 4; Conservation
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les 4; Conserv
                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                        3 GLSI 6
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STREET: 2029 Century Park East,
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                      Kurt A. MacLean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-07-03
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                                                                   Products and
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                                                                                                                                                                                                                                                                                                                  Score 18;
Pred. No. 1
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Pred. No.
                                                                                                                                                                                                                                                                                                  Mismatches
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                                                              Methods for Their Production
Suite 3800
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Query Match
Best Local Similarity
"here 4; Conserve
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                                                                                                                                                                                                                                                                              Sequence 49, Application User Patent No. US20020131975A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-953-510-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 48: SEQUENCE CHARACTERISTICS:
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                             APPLICANT: Horwitz, Marcus A.
TITLE OF INVENTION: Abundant Extracellular
Products and Methods for Their Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MacLean, Kurt A.
REGISTRATION NUMBER: 31,118
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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FILING DATE: 23-MAY-1995
APPLICATION NUMBER: US 08/289,667
FILING DATE: 12-AUG-1994
APPLICATION NUMBER: US 08/156,358
FILING DATE: 23-NOV-1993
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                            COUNTRY: U.S.A.
                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                            STREET: 2029 Century Park East,
                                                                                                                                                                 ADDRESSEE: Kurt A. MacLean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: Erdman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                     Application US/09953510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (310) 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/953,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 18; DB 10; ilarity 100.0%; Pred. No. 1.6e+02; Conservative 0; Mismatches 0;
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                                                                                                                                               Suite 3800
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                                                                                                                                                                                                                    and Use
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STRAIN: Erdman SEQUENCE DESCRIPTION: SEQ ID NO: 49: US-09-953-510-49
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US-10-147-255-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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TELEFAX: (310) 277-1297
INFORMATION FOR SEO ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/289,667
FILING DATE: 12-AUG-1994
APPLICATION NUMBER: US 08/156,358
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MACLEAN, KUIT A.
REGISTRATION NUMBER: 31,118
REFERENCE/DOCKET NUMBER: 112-272
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-CENSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: Flam PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

Version #1.30
                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/147,255
EILING DATE: 15-May-2002
CLASSIFICATION: - CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Kurt A. MacLean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/226,539A
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Horwitz, Marcus A.

ITLE OF INVENTION: Abundant Extracellular

Products and Methods for Their Production and Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GLSI 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/447,398 FILING DATE: 23-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/953,510 FILING DATE: 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                   STREET: 2029 Century Park East, Suite 3800
                                                                                                                                                                                                                                                     90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                      U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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US-10-147-255-49
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 49, Application US/10147255 publication No. US20030152584A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPOSITION

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Kurt A.
                                                                                                                                                    APPLICATION NUMBER: US/10/147,255
FILING DATE: 15-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                       Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HORWITZ, Marcus A.
TITLE OF INVENTION: Abundant Extracellular
Products and Methods for Their Production and Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 GLSI 13
                            APPLICATION NUMBER: US/09/226,539A FILING DATE: CUNKNOWN> APPLICATION NUMBER: US 08/447,398 FILING DATE: 23-MAY-1995 APPLICATION NUMBER: US 08/289,667 FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2029 Century Park East, Suite 3800
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
               APPLICATION NUMBER:
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Kurt A. MacLean

US 08/156,358

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; SEQUENCE DESCRIPTION: SEQ ID NO: 48: US-10-147-255-48
                                                                                                                                                                                                                                                                                                      TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                      NAME: MACLEAN, KUTT A.
REGISTRATION NUMBER: 31,118
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 277-1297
                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: internal
                                                                                                                                                                                                                                     TOPOLOGY: linear
1 GLSI 4
                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/447,398 FILING DATE: 23-WAY-1995 APPLICATION NUMBER: US 08/289,667 FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/156,358 FILING DATE: 23-NOV-1993
                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis
                                     Conservative
                                                 100.0%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <Unknown>
                                       0
                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           112-272
                                                         1.6e+02
                                                                       DB 12;
                                                                         Length 15
                                          Indels
                                          0
                                          Gaps
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APPLICANT: Katz, Lawrence C.

APPLICANT: Katz, Lawrence C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING

TITLE OF INVENTION: CELL DEATH

FILE REFERENCE: 10001-005-999

CURRENT PRICE SECTION NUMBER: US/09/922,261

CURRENT PRILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: US/09/461,697

PRIOR FILING DATE: 1999-12-14

NUMBER OF SEQ ID NOS: 466

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 99

LENGTH: 16

TYPE: PRT

CURRENT: Homo Sapiens
               RESULT 9
US-09-813-333-66
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                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-922-261-99
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Sequence 66, Application US/09813333
                                                                                                                                                        Matches
                                                                                                                                                                        Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: COGENT NEUROSCIENCE, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (310) 788-50
TELEPAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 112-272 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MacLean, Kurt A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99, Apprical 11471A1 0. US200201111471A1
                                                                                                                    1 GLSI 4
                                                                                                                                                     4,
                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GLSI 4
                                                                                      GLSI 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lo, Donald C.
Barney, Shawn
Thomas, Mary Beth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Portbury, Stuart D.
Puranam, Kasturi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09922261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MacLean, Kurt A. REGISTRATION NUMBER: 31,118
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                 100.0%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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Pred. No. 1.6e+02;
                                                                                                                                               Mismatches
                                                                                                                                                                 1.8e+02;
                                                                                                                                                                             Length 16;
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 15;
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                                                                                                                                            0;
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RESULT 11
US-09-880-748-2186
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                                                                                                         Sequence 2186, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
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APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CHERENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-813-333-66
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2174, Application US/09880748 Publication No. US20030059937A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PF523
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DeGroot, Anne S
TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
FILE REFERENCE: 17999-004 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 16
TYPE: PRT
                                                                                                                                                                                                                                        3 GLSI 6
                                                                                                                                                                                                                                                                          1 GLSI 4
                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                           Score 18;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                           1.8e+02;
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                                                                                                                                                                                                                                                                                                  Gaps
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APPLICATION NUMBER: 60/212,210

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Query Match
Best Local Similarity
Watches 4; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens US-09-880-748-2980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunosp
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
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                                                                                                                                                         US-09-991-225-61
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PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2980, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2186
Sequence 61, Application US/09991225
Publication No. US20030153063A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HI
TITLE OF INVENTION: HEART AND VARIANTS THEREOF
FILE REFERENCE: D0075.NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 2980
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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CURRENT APPLICATION NUMBER: US/09/991,225
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/249,613
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/305,818
PRIOR APPLICATION NUMBER: 60/305,818
PRIOR PILING DATE: 2001-07-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 62
RESULT 15
US-09-991-225-73
; Sequence 73, Application US/09991225
; Publication No. US20030153063A1
; Publication No. US20030153063A1
; GENERAL INFORMATION:
APPLICANT: BISTACL MYCET SQUIDD COMPANY
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED;
TITLE OF INVENTION: HEART AND VARIANTS THEREOF
; FILE OF INVENTION: HEART AND VARIANTS THEREOF
; FILE OF INVENTION: HEART US/09/991,225
; CURRENT APPLICATION NUMBER: US/09/991,225
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR PELING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
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; Sequence 62, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/257,611
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/305,818
PRIOR FILING DATE: 2001-07-16
NUMBER OF SEQ ID NOS: 81
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Matches 4
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TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED
TITLE OF INVENTION: HEART AND VARIANTS THEREOF
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CURRENT FILING DATE: 2001-11-16
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and is derived by analysis of the total score distribution.
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Match
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

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PCT-US02-27760-142

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PCT-US02-27760-197

PCT-US02-27760-377

PCT-US02-27760-377

PCT-US02-27760-377

PCT-US02-27760-377

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PCT-US02-27760-387

PCT-US02-27760-387

US-10-631-441-2489

US-10-631-441-2654

US-10-631-441-2654

US-10-588-898A-2654

US-10-603-113-23802

US-10-603-113-23802

US-10-603-113-23802

US-10-603-114-6279

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
     Sequence
       730, App
350, App
406, App
1524, App
196, App
275, App
275, App
2768, App
2768, App
2489, App
26551, App
26554, App
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2768, App
2776, App
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18 100.0 79 6 US-10-603-113-26666 18 100.0 81 6 US-10-603-113-2166 18 100.0 81 6 US-10-603-113-2116 18 100.0 83 6 US-10-603-113-21820 18 100.0 85 6 US-10-603-113-23917 18 100.0 97 6 US-10-603-113-23917 18 100.0 97 6 US-10-603-113-22075 18 100.0 97 6 US-10-603-113-17866 18 100.0 97 6 US-10-603-113-2585 18 100.0 97 6 US-10-603-113-2585 18 100.0 98 6 US-10-603-113-2585 18 100.0 99 6 US-10-603-113-2585 18 100.0 99 6 US-10-603-590-202 18 100.0 100 6 US-10-603-590-202	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	-
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	14336, A	ddy Yor	142, App	25585, A	21294, A	141, App	17866, A	79; Appl	68, Appl	2, Appli	22075, A	5684, Ap	-	-	21820, A	23903, A	21166, A	26666, A	

## ALIGNMENTS

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RESULT 2 PCT-US02 Sequen GENERA APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI TITLE TITLE TITLE TURE	Qу	Query M Best Lo Matches	; LE ; TYI ; OR ; PCT-US	CURI CURI PRIC PRIC NUM SOF	; APPI ; APPI ; TITI ; TITI ; FILI	PCT-US( ; Seque; ; GENEI; ; APPI ; APPI
-277 Ce 1 L IN CANT CANT CANT CANT CANT CANT CANT CAN	1 GLSI 4      1 GLSI 4	atch cal Similarity 4; . Conservat	; LENGTH: 6 ; TYPE: PRT ; ORGANISM: Homo sapiens PCT-US02-27760-730	CURRENT APPLICATION NUMBER: PCT/US02/27760 CURRENT FILING DATE: 2003-07-21 PRIOR APPLICATION NUMBER: US 60/316,664 PRIOR FILING DATE: 2001-08-31 NUMBER OF SEQ ID NOS: 736 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 730	APPLICANT: HADERT, MARY APPLICANT: HADERT, Rene S. APPLICANT: Jakobovits, Aya APPLICANT: Jakobovits, Aya TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND FILE REFERENCE: 511582004340	PCT-US02-27760-730; Sequence 730, Application PC/TU; GENERAL INFORMATION: APPLICANT: Agensys, Inc.; APPLICANT: Challita-Eid, Pia; APPLICANT: Raitano, Arthur B.
60-142 42, Application PC/TUS0227760 42, Application PC/TUS02/27760 FENCE: 511582004340 FPLICATION HUMBER: PCT/US02/27760 FILING DATE: 2003-07-21		.0%; Score 18; .0%; Pred. No. 0; Mismatcl		BER: PCT/US02/27760 003-07-21 R: US 60/316,664 -08-31 36 1ndows Version 4.0	: Faris, Mary : Hubert, Rene S. : Jakobovits, Aya : Jakobovits, Aya : INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT RENCE: 511582004340	730 Application PC/TUS0227760 AMATION: gensys, Inc. Challita-Eid, Pia M. Raitano, Arthur B.
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RESULT 4
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-USO2-27760-142
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
SEQ ID NO 406
                                                             APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: ENUTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE OF INVENTION: ENUTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582004340
CURRENT FILING DATE: 2003-07-21
CURRENT FILING DATE: 2003-07-21
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PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 736
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 350
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APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eld, Pia M.
APPLICANT: Raitano, Arthur B.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 142
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               SOFTWARE: FastSEQ for Windows Version 4.0
                                       NUMBER OF SEQ ID NOS: 736
                                                      PRIOR APPLICATION NUMBER: US 60/316,664
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                               APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
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APPLICANT: Hubert, Rene S.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT &
FILE REFERENCE: 511582004340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: PCT/US02/27760 CURRENT FILING DATE: 2003-07-21
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Local Similarity 100.0%;
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Pred. No. 1
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; ORGANISM: Homo sapiens PCT-US02-27760-157
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                                    NUMBER OF SEQ ID NOS: 736
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 157
LENGTH: 10
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 524
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Best Local :
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APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT I
FILE REFERENCE: 511582004340
CURRENT APPLICATION NUMBER: PCT/US02/27760
CURRENT FILING DATE: 2003-07-21
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Best Local Similarity
                                                                                                                                PRIOR APPLICATION NUMBER: US 60/316,664 PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                           APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Rattano, Arthur B.
APPLICANT: Faris, Mary
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APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: UUCLETC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582004340
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APPLICANT: Challita-Eic
APPLICANT: Raitano, Art
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TYPE: PRT
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100.0%; Pred. No. 1
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Pred. No.
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CURRENT APPLICATION NUMBER: PCT/US02/27760
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 60/316,664
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEO ID NOS: 736
SOFTWARE: FASTSEQ for Windows Version 4.0
SEO ID NO 275
LENGTH: 10
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Sequence 196, Application PC/TUS0227760
; Sequence 196, Application PC/TUS0227760
; GENERAL INFORMATION:
   APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faits, Mary
APPLICANT: Hubert, Rene S.
; APPLICANT: Jakobovits, Aga
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 205P185 USEFUL IN TREATMENT AND DETECTION OF CANCER
; TITLE OF INVENTION NUMBER: PCT/US02/27760
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 60/316,664
; PRIOR FILING DATE: 2001-08-31
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Best Local Similarity
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PCT-US02-27760-275
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 196
LENGTH: 10
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challite-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
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                                    Matches
                                                                   Query Match
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APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582004340
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Local Similarity 100.0%; Pred. No.
hes 4; Conservative 0; Mismatch
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                                                      Score 18; DB Pred. No. 20;
                                                                       DB 1; Length 10;
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     RESULT 11
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Best Local Similarity
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APPLICANT: Hubert, Rene S.

APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582004540
CURRENT APPLICATION NUMBER: PCT/US02/27760
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 66/316,664
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 736
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 377
LENGTH: 10
TYPE: PRT
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PCT-US02-27760-377
                                                                                                     SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 394
LENGTH: 10
TYPE: PRT
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APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P185 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582004340
CURRENT APPLICATION NUMBER: PCT/US02/27760
CURRENT FILING DATE: 2003-07-21
                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/316,664
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 736
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Agensys, Inc. APPLICANT: Challita-Eic
                                                                                      ORGANISM: Homo sapiens
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Raitano, Arthur B.
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Pred. No.
                  Score 18;
Pred. No.
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                  DB 1;
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RESULT 13
US-10-411-206A-11
(Sequence 11, Application US/10411206A
; Sequence 11, Application US/10411206A
; GENERAL INFORMATION:
APPLICANT: ITVING W. WAINER et al.
FITLE OF INVENTION: COMPUTER-BASED MODEL FOR IDENTIFICATION AND CHARACTERIZATION FOR TITLE OF INVENTION: NON-COMPUTER-BASED MODEL FOR NICOTINIC ACETYLCHOLINE RECEPTORS;
TITLE OF INVENTION: AND RELATED LIGAND-GATED ION CHANNEL RECEPTORS
FILE REFERENCE: 1173-1025p
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GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/10/462,850
CURRENT FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 2168
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CURRENT APPLICATION NUMBER: US/10/411,206A CURRENT FILING DATE: 2003-11-04
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Best Local Similarity
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CURRENT FILING DATE: 2003-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hubert, Rene S.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582004340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/316,664 PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Agensys, Inc
APPLICANT: Challita-Eic
APPLICANT: Raitano, Art
                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: sequence located in PMEL17 OR D12S53E at 164-173 and OTHER INFORMATION: Sequence 2167 in this patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-462-850-2168
equence 2168, A
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Similarity 100.0%;
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Pred. No.
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Best Local
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SOFTWARE: Patent.pm
SEQ ID NO 2489
       Matches
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LENGTH: 23
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PRIOR APPLICATION NUMBER: US 08/905,223
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,135
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 08/905,133 PRIOR FILING DATE: 1997-08-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/631,402 CURRENT FILING DATE: 2003-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: Expressed Sequence Tags and Encoded
                                                                                           OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: GEN-T119C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dumas Milne Edwards, Jean Baptiste
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SOFTWARE: PatentIn versi
                                                                                                                                               LOCATION: -21
                                                                                                                                                                NAME/KEY: SIGNAL
                                                                                                                                                                                    OTHER INFORMATION: Prostate FEATURE:
                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: OTHER INFORMATION:
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     Conservative
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score 4.50
seq SILFHCSVCLFLC/QY
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                    100.0%; Score 18; 100.0%; Pred. No.
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RESULT 15

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J Sequence 2489, MINCREANINE
GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: NEWENION: Expressed Sequence Tags and Encoded Human Proteins
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
FILL REPERBURE: GEN-T1991

PRIOR PRICE TILLS DATE: 1997-08-01

PRIOR APPLICATION NUMBER: US 08/905,134

PRIOR PRICE TILLS DATE: 1997-08-01

PRIOR PRICE TILLS DATE: 1997-08-01

PRIOR APPLICATION NUMBER: US 08/905,79

PRIOR APPLICATION NUMBER: US 08/905,79

PRIOR APPLICATION NUMBER: US 08/905,79

PRIOR APPLICATION NUMBER: US 08/905,134

PRIOR PRICE TILLS DATE: 1997-08-01

PRIOR APPLICATION NUMBER: US 08/905,134

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r cell receptor be hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote major glycoprotein nitrogen probable rical prote probable rical prote 40% ribosomal prote hypothetical protein - Rhi per Japan hypothetical protein - Rhi protein - Sain hypothetical 
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T cell receptor beta chain V region
C;Species: Homo sapiens (man)
               F.G.
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E96034	T12859	T04575	CCBM6	H49846	AI0316	C31684	C86629	AH0619	T04176	B44479	в90530	AD0925	T30790	A42508	A60007
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## ALIGNMENTS

human (fragment)

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submitted to GenBank, June 2000 A;Anthors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fraction a;Anthors: Ferreira, V.C.A.; Ferro, J.A.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins chado, M.A.; Madeira, A.M.B.; Markino, C.F.M.; Miracca, E.C.; Miyaki, C A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,	A;Cross-references: GB:AE003870; GB:AE003849; NID:g9104955; PIDN:AAF82976.1; GSPDB:GN-A;Experimental source: Strain 945c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrerlas-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.	Nature 406, 151-157, 2000  A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  A;Reference number: A82515; MUID:20365717; PMID:10910347  A;Note: for a complete list of authors see reference number A59328 below  A;Accession: G82839  A;Accession: G82839  A;Rolecule type: DNA  A;Residues: 1-31 <sim></sim>	RESULT 2  RESULT 2  Apportmentical protein XF0163 [imported] - Xylella fastidiosa (strain 9a5c)  Apportmentical protein XF0163 [imported] - Xylella fastidiosa (strain 9a5c)  C; Species: Xylella fastidiosa C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C; Date: 18-Aug-8000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C; Accession: G82839 C; Accession: G82839 R; Apportments. The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq	Qy ' 1 GLSI 4 Db 6 GLSI 9	Query Match 100.0%; Score 18; DB 2; Length 17; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Accession: 50/019 A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-17 <bur> A;Cross references: EMBL:Z49930; NID:g887494; PIDN:CAA90176.1; PID:g887495 C;Keywords: T-cell receptor</bur>	C;Species: Homo Sapiens (man) C;Date: ID-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999 C;Date: ID-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999 C;Accession: S57519 R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaet, V.P. submitted to the EMBL Data Library, June 1995 A;Description: T cell receptor repertoire for a viral epitope in humans is diversifie A;Reference number: S57494 A;Reference number: S57494

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submitted to the EMBL Data I:
A; Reference number: Z19189
A; Accession: T19865
A; Status: preliminary; trans:
A; Molecule type: DNA
A; Residues: 1-34 <WIL>
A; Cross-references: EMBL: Z81.
A; Experimental source: clone
C; Genetics:
A; Gene: CESP:C40H5.1
A; Experimental source: C; Genetics: A; Gene: CESP:H12D21.1; A; Map position: 5
                                                                                  A; Molecule type: DNA
A; Residues: 1-34 <WI2>
                                                                    A; Cross references:
                                                                                                             A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                    submitted to the EMBL Data Library, A;Reference number: Z20387
A;Accession: T27557
                                                                                                                                                                                                                                                                                                                                                 hypothetical protein H12D21.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T23074; T27557
                                                                                                                                                                                     A; Experimental source: clone H12D21
R; Ainscough, R.
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A;Residues: 1-34 <WIL>
A;Cross-references: EMBL:292849; PIDN:CAB07428.1;
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A;Reference number: Z19671
A;Accession: T23074
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T19865
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tc
C;Accession: T19865
R;White, S.
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A;Contents: annotation
C;Genetics:
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                                          EMBL:278067; PIDN:CAB01526.1; GSPDB:GN00023; CESP:2C412.7
Se: clone 2C412
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               CESP: ZC412.7
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A.L.; Z
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C; Accession: S68648
R; Calvete, J.J.; Dostalova, Z.; FEBS Lett. 379, 207-211, 1996
                                                                                RESULT 7
S68648
                                  major glycoprotein PSP-I - pig (fragments)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 17-Mar-1999
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A; Residues: 1-34 <WIL>
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C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T27560
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A; Molecule type: DNA
A; Residues: 1-34 <WIL>
A; Cross-references: EMBL: 278066; PIDN: CAB01519.1;
A; Cross-reference: clone W06A7
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A; Map position: 5
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ches 0;
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           Thole, H.H.; Toepfer-Petersen
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hypothetical protein ORF35 - Norway spruce chloroplast C; Species: chloroplast Picea ables (Norway spruce) C; Species: chloroplast Picea ables (Norway spruce) C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999 C; Accession: T11812 R; Kluemper, S.; Kanka, S.; Riesner, D.; Etscheid, M. submitted to the EMBL Data Library, March 1997 A; Description: Characterisation of a Norway spruce chloroplast DNA clone: Complete A; Accession: T11812 A; Accession: T11812
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A; Genome:
C; Keywords
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A; Residues: 1-7; 8-12; 13-20; 21-27; 28-32; 33-34
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A;Residues: 1-35 <KLU>
A;Cross-references: EMBL:U92462; NID:g2959581; PID:g2959588
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                                                                                                                                                                                                                                                                                                                                                                                                               probable nitrogen regulation protein II (EC 2.7.3.-) - Xanthomonas campestris
C:Species: Xanthomonas campestris pv. campestris
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 17-Jul-1998
C:Accession: S11913
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RESULT 10
S78726
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A;Title: Use of oligonucleotide probes to identify members of A;Reference number: S11912; MUID:91042416; PMID:2233675
A;Accession: S11913
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A; Residues: 1-46 < OSB>
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Best Local
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Best Local
                                                                                                                                                                                                              Superfamily: glnL regulatory protein II; sensor histidine kinase homology;
Keywords: ATP; autophosphorylation; phosphohistidine; phosphoprotein; phosphotransfer;
;1-41/Domain: sensor histidine kinase homology (fragment) <SHK>
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$68648; MUID:96184566; PMID:8603690
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Pred. No. 2.3
0; Mismatches
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protein YKL162c-a - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 15-Jan-1999
C;Accession: S78726
C;Accession: S78726
R;Yandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.
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C;Genetics:
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A; Residues: 1-50 <VA2>
A; Cross-references: EMI
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Plant Mol. Biol. 27, 1043-1052, 1995
A; Title: Gibberellin-regulated expression:
A; Reference number: $56638; MUID:95284341;
A; Accession: $56727.
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C;Date: 27-Oct-1995 #sequence_revision
C;Accession: S56727
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                                                                                                                                                                                                                               hypothetical protein asr3001 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec C;Accession: AB2181
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AB2181
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                                                                                                                                                          R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentou
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A; Residues: 1-53 <HUT>
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             A;Cross-references: GB:BA000019; PIDN:BAB74700.1; A;Experimental source: strain PCC 7120 C;Genetics:
                                                                                                    A; Reference number: AF
A; Accession: AB2181
A; Status: preliminary
                                                                   A; Molecule type: DNA
A; Residues: 1-55 < KUR>
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Best Local
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                                                                                                                                            AB1807;
                                                                                                                                              Sequence of the Filamentous Nitrogen-fixing Cyanobacterium 7; MUID:21595285; PMID:11759840
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Pred. No. 3.5
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ase, March 1994
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                                                       PID:g17132095; GSPDB:GN00179
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M.; Yamada, M.; Yasuda, M.;
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RESULT 15
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A;Experimental source: strain TIGR4
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H95182
                                                                                                                                                                                                                                                                         A; Molecule type: DNA A; Residues: 1-56 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                               on, J.D.; Umayam, L.A.; Wh. nson, T.; Hickey, E.K.; Ho Science 293, 498-506, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein SP1570 [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae (c;Species: Streptococcus pneumoniae (c;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 C;Accession: H95182
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A; Accession: H95182
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A:Genome: nucleomorph
C:Superfamily: Escherichia coli ribosomal protein S14
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A:Molecule type: DNA
A:Residues: 1-56 <DOU>
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Nature 410, 10
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                                                                                                                       Conservative
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ilarity 100.0%;
Conservative 0.
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#sequence_revision 10-May-2001 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                      K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei
White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
Holt, I.E.
                                                                                                                                     100.0%;
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Search completed: August 20, 2003, 12:42:18 Job time: 5.79518 secs

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J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.; Title: Genome of the Bacterium Streptcoccus pneumoniae Strain R6.
                                                                                                                                                                           A;Gene: spr1428
                                                                                                                                                                                                A;Cross-references: GB:AE007317; PIDN:AAL00232.1; PID:g15459082; GSPDB:GN00174
                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein spr1428 [imported] - Streptococcus pneumoniae (strain R6) c;Species: Streptococcus pneumoniae C;Spate: 22-Oct_2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-56 <KUR>
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VX2A\_CVPPU P09046; 01-NOV-1988 01-NOV-1988 15-SEP-2003 X2A.protein.

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Porcine transmissible gastroenteritis coronavirus

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01-FEB-1991
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                                                                                                                                                                                                                                                                    Goebel S.J., Johnson Paoletti E.;
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InterPro; IPR006784; Corona_3.
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Biochimie 69:591-600(1987).
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                                      STRAIN-UAB CTIP;
STRAINE=21267165; Por Chamband T
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15-SEP-2003
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                        Chambaud I., Heilig R.
Moszer I., Dybvig K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccinia virus (
Viruses; dsDNA v
Orthopoxvirus.
Mycoplasma
                   Moszer I., Dy Blanchard A.;
                                                                                                                                                          Q98R64;
                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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01-APR-1993
01-APR-1993
       "The complete genome
                                                                                         Mycoplasma pulmonis.
Bacteria; Firmicutes;
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MYPU_1460:
                                                                                 NCBI_TaxID=2107;
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                                                                                                                                                                                                                                                                                                                                                                                                               Mikryukov N.N., Chizhikov V.E., Prikhod'Ko G.
Serpinskii O.I., Blinov V.M., Nikulin A.E., V
                                                                                                                                                                                                                                                                                                                                                                                      Biotekhnologiya 4:442-449(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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viruses, no RNA
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ig R., Ferris S.,
K., Wroblewski H
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Pred. No.
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      murine respiratory pathogen
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                    the European Bioinformatics Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. Usentities requires a license agreement 'cor send an email to 'cor send an em
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MypuList; MYPU_1460; -.

HAMAP; MF_00363; -; 1.

InterPro; IPR005359; UPF0154.

Piam; PF03672; UPF0154; 1.

ProDom; PD048972; UPF0154; 1.

Hypothetical protein; Transmembrane; Complete proteome.
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28+FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Endothelial lipase (EC 3.1.1.3) (Endothelial-derived lipase)
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-I- SIMILARITY: BELONGS TO THE UPF0154 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BN-Lx/Cub, and SHR/OlaIpcv;
MEDLINE-21913086; PubMed-11924532;
MEDLINE-21913086; PubMed-11924532;
Meonne A.C.M., den Bleman M.G., van Lith H., van Zutphen B.F.M.;
Bonne A.C.M., den Bleman M.G., van Lith H., van Zutphen B.F.M.;
"Sequencing and chromosomal assignment of the rat endothelial-derived
"Sequencing and chromosomal assignment of the rat endothelial-derived
lipase gene (Lipg).";
DNA Seq. 12:285-287(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chorv
Mammalia; Eutheria; Rode
MCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq. 12:285-287(2001).
FUNCTION: Has phospholipase and triglyceride lipase activities.
Hydrolyzes high density lipoproteins (HDL) more efficiently than
other lipoproteins. Binds heparin (By similarity).
CATALYTIC ACTIVITY: Triacylglycerol + H(2)0 = diacylglycerol + a
                                                                                                                                                                                                                                                                                                                                                       fatty acid anion.
SUBCELLULAR LOCATION: Secreted (By similarity).
MISCELLANBOUS: It is termed endothelial lipse due to the fact
that it is synthesized in endothelial cells, a characteristic that
distinguishes it from other members of the family. However this
protein is also expressed in other cell types.
SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 GLSI 15
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                                             equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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Pred. No.
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PIR; C31684; C31684.
Hypothetical protein.
SEQUENCE 83 AA; 9512 MW;
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P22054;
01-AUG-1991
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Pfam; PF00151; lipase; 1.
Hydrolase; Lipid degradation
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01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical protein IORF2.
Bovine coronavirus (strain Mebus) (BCOV) (BCV),
Bovine coronavirus (strain Quebec) (BCOV) (BCV),
Viruses; ssRNA positive-strand viruses, no DNA s
Coronaviridae; Coronavirus.
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Kienzle T. E., Abraham S., Hogue B.G., Brian
"Structure and orientation of expressed bovi
hemagglutinin-esterase protein.";
J. Virol. 64:1834-1838(1990).
                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     Parker M.D., Cox G.J., Deregt D., Fitzpatrick D.R., E "Cloning and in vitro expression of the gene for the haemagglutinin glycoprotein of bovine coronavirus."; J. Gen. Virol. 70:155-164(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91353426; PubMed-2103108;
Kienzle T.E., Abraham S., Hogue B.G.,
"Structure and expression of the bovi
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AY027562; AAK14775.1;
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ilarity 100.0%;
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InterPro; IPR006312; TatA_E.
Pfam; PF02416; MttA_Hcf106; 1.
TIGRFAMS; TIGR01411; tatAE; 1.
                                                                                                                                                                                                                                                         EMBL; AJ414153; CAC92840.1; EMBL; AE013720; AAM84747.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quall M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Genome sequence of Yersinia pestis, the causative agent of plagnature 413:523-527(2001).
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yersinia pestis,
Bacteria, Proteobacteria;
Enterobacteriaceae, Yersin
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                                                                                                                                                                                                                                                                                                                               a and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce, an email to license@isb-sib.ch).
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buchrieser C., Glaser P., Rusnick C., Ne
Kunst F., Sansonetti P., Parsot C.;
"The virulence plasmid pWR100 and the rep
by the type III secretion apparatus of Si
Mol. Microbiol. 38:760-771/2nnn
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P40705; O55297;
01-FEB-1995 (Rel. 3
01-FEB-1995 (Rel. 3
28-FEB-2003 (Rel. 4
                                                                                                                                                                                                                                                                                                            SPECIES-S.flexneri; STRAIN-301 / Serotype MEDLINE-22272406; PubMed-12384590; Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Yang J., Yang F., Zhang X., Zhang J., Yang Sun L., Xue Y., Zhao A., Gao Y., Zhu J., K Cheng H., Yao Z., He B., Chen R., Ma D., C
                       SEQUENCE
                                                                                  requires
                                                                                                        Venkatesan M.M., Buysse J.M.,
"Surface presentation of Shig
                                                                                                                                             MEDLINE=92193289; PubMed=1312536;
                                                                                                                                                                     SPECIES=S.flexneri;
                                                                                                                                                                                             SEQUENCE OF 1-53
                                                                                                                                                                                                                                      Nucleic
                                                                                                                                                                                                                                                          through
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasakawa C., Komatsu K., Tobe T., Suzuki T., Yoshikawa M., "Eight genes in region 5 that form an operon are essential invasion of epithelial cells by Shigella flexneri 2a."; J. Bacteriol. 175:2334-2346(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=S.flexneri; STRAIN=YSH600
MEDLINE=93224456; PubMed=8385666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete DNA sequence and Shigella flexneri.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=S.flexneri; STRAIN=M90T / MEDLINE=21189246; PubMed=11292750
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Bacteria; Proteobacteria; Gammapro:
Enterobacteriaceae; Shigella.
NCBI_TaxID=623, 624;
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                                                                                                                                                                                                                            sequence of Shigella flexneri 2a: insights into comparison with genomes of Escherichia coli K12 Acids Res. 30:4432-4441(2002).
                     FROM
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                                                          presentation of Shigella flexneri
the products of the spa locus.";
riol. 174:1990-2001(1992).
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g J., Yang G., Wu H.
Zhu J., Kan B., Dir
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Qu D., Dong J.,
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"Comparison and high conservation of nucleotide sequences of spa-mx:

regions between S. sonnel and S.flexneri -- identification of a new
gene coding plausible membrane protein.";

Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-1995) FOR SUBFACE PRESENTATION OF INVASION PLASMID

ANTIGENS. COULD PLAY A ROLE IN PRESERVING THE TRANSLOCATION

ANTIGENS. COULD PLAY A ROLE IN PRESERVING THE TRANSLOCATION

COMPETENCE OF THE IPA ANTIGENS. REQUIRED FOR INVASION AND FOR
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01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update
Cytochrome C6 (Soluble cytochrome f) (Cytoc
553).
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EMBL; D50601; BAA09163.1; ALT_INIT.
PIR; H49846; H49846.
Interpro; IPR002191; Bac_export_3.
Interpro; IPR006306; HrpO.
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                                                                                                                                                                    SEQUENCE, AND CHARACTERIZATION.
MEDLINE=88139277; PubMed=3481367;
Okamoto Y., Minami Y., Matsubara H., Sugimura Y.;
Pstudles on algal cytochromes VI: some properties and sequence of cytochrome c6 from a green alga, Bryopsis J. Blochem. 102:1251-1260(1987).
                                                                                                                                                                                                                                                                                                                                                                                              Bryopsis maxima (Green alga).
Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
Bryopsidaceae; Bryopsis.
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PRINTS; PR00952; TYPE3IMOPROT.
TIGRFAMs; TIGRO1403; fl1Q_rel_IJ
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-i- SÜBUNIT: Monomer.
-i- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
-i- PTM: Binds one heme group per molecule.
-i- MISCELLANEOUS: The midpoint redox potential for this protein i
                                                                                                               -I- FUNCTION: Functions as an electron carrier be
cytochrome b6f and photosystem I in oxygenic
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3129;
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SUBCELLULAR LOCATION: Integral membrane protein ()
SIMILARITY: BELONGS TO THE FLIQ/MOPD/SPAQ FAMILY.
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403; fliQ_rel_III; 1.
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552D3DBCB9C896E3 CRC64;
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Pred. No. 2.8e+0;
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P22407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00034; cytochrome_c; 1.
PRINTS; PR00605; CYTCHROMECIC.
PRINTS; PR00607; CYTCHROMECIE.
PROSITE; PS00190; CYTOCHROME_C; 1.
Electron transport; Photosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003088; Cyt_CI.
InterPro; IPR002329; Cyt_CIC.
InterPro; IPR002323; Cyt_CIE.
InterPro; IPR000345; CytC_heme_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SIMILARITY: Belongs
PIR; A30021; CCBM6.
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P08197;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
                                                                                                                              EMBL; M21778; AAA88409.1; PIR; F31844; F31844.
                                                                                                                                                                                                                                                            "Complete nucleotide sequence of the Streptomyces lividans pIJ101 and correlation of the sequence with genetic propert J. Bacteriol. 170:4634-4651(1988).
                                                                                                                                                                                                                                                                                                           MEDLINE-89008081; PubMed-3170481; Kendall K.J., Cohen S.N.;
                                                                                                                                                                                                                                                                                                                                                          Streptomycineae;
NCBI_TaxID=1916;
                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces lividans. Plasmid pIJ101.
                                                                                                                                                                                                                                                                                                                                                                                                                      SPDA.
                                                                                             SEQUENCE
                                                                                                                   Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                               Protein spdA
                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 GLSI 47
83 GLSI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GLSI 4
                       1 GLSI 4
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                                                         Similarity
                                                                                                        Transmembrane.
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nilarity 100.0%;
Conservative 0
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                                               Conservative
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HEME (COVALENT).
IRON (HEME AXIAL LIGAND).
IRON (HEME AXIAL LIGAND).
EFDE2C2680175E01 CRC64;
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Pred. No.
                                              Score 18; DE
Pred. No. 3.1
0; Mismatches
                                                                                              47D80CB57D824656 CRC64;
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. 2.9e+02;
0;
                                                           3.1e+02;
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                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 88
                                                                     Length 94;
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properties.";
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RESULT 12
GRP7_DAGE
ID GRP7_D
ID GRP7_D
AC P37704
DT 01-OCT
DAGE
CO Sperma
OC ASTERI
OX NCBI_T
RN 11]
RP SEQUEN
RR Aleith
RT Gene
RT Gene
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         RESULT 13
NULM_CERCA
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
    SEQUENCE FROM N.A.
STRAIN-Guatemala laboratory colony;
MEDLINE-95261546; PubMed-7742977;
Gasparich G.E., Sheppard W.S., Han
                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Tephritoidea; Tephritidae; Ceratitis.
                                                                                                                                                                                                                                                                034049;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
NADH-ubiquinone oxidoreductase chain 4L (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P37704;
01-OCT-1994 (Rel. 3
01-OCT-1994 (Rel. 3
01-OCT-1994 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat;
SIGNAL
                                                                                                                                                                                                                              Ceratitis capitata (Mediterranean fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                   NULM_CERCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1994 (Rel. 30, Last annotation
Clycine-rich protein DC7.1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X15706; CAA33736.1; -. PIR; S35715; S35715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
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-i- FUNCTION: MAY BE CONNECTED WITH THE INITIATION OF EMBRYOGENESIS OR WITH THE METABOLIC CHANGES PRODUCED BY THE REMOVAL OF AUXINS.

-i- DEVELOPMENTAL STAGE: TRANSIENTLY EXPRESSED DURING EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Daucus carota (Carrot).

Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; Campanulids; Apiales; Apiaceae; Daucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Gene expression during induction cell suspensions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aleith F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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ilarity 100.0%;
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  Sheppard W.S.,
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7C00D44637B7A364 CRC64;
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GLYCINE-RICH PROTEIN DC7.1.
2 APPROXIMATE REPEATS OF H-H-G(4,6)-H.
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18;
Pred. No.
  Han H.Y.,
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  McPheron
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В.А.,
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  Steck G.J.;
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RESULT 14
NULM_DROME
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Best Local S
Matches 4
                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                         J. Mol. Evol. 51:48-63(2000).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone =
                                                                                                                                                                                                                     STRAIN=Oregon-R, and Zimbabwe 53; MEDLINE=20363871; PubMed=10903372;
                                                                                                                                                                                                                                                                                                                                   STRAIN=Bretagne;
MEDLINE=88212147; PubMed=3130291;
                                                                                                                                                                        Drosophila melanogaster subgroup.";
                                                                                                                                                                                                         Ballard J.W.O.;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                evolutionary considerations.";
Genetics 118:649-663(1988).
                                                                                                                                                                                                                                                                                                                             Garesse
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
02-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003214; Oxidred4L.
Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                         "Comparative genomics of mitochondrial DNA in
                                                                                                                                                                                                                                                                                                                                                                                                                            Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MT:ND4L OR ND4L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NADH ubiquinone oxidoreductase chain 4L (EC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P18934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; NAD; Ubiquinone; Mitochondrion. SEQUENCE 96 AA; 11346 MW; B743137D69FF2331 CRC64;
                                                                                                                                                                                                                                                                                                           "Drosophila melanogaster mitochondrial DNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U12925; AAA85798.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NULM_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic molecular markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insect Mol. Biol. 4:61-67(1995).
-i - CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  capitata) populations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Analysis of mitochondrial DNA and development diagnostic molecular markers for Mediterranean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 GLSI 77
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Pred. No.
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                                                                 There are no rest
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era; Muscomorpha;
                                     http://www.isb-sib.ch/announce/
                                                                                                                                  NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                           gene organization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6.5.3).
                                                    Usage
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M37275;

AAA69712.1;

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RESULT 15
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ID WULMCDROYA
AC P07708
DT 01-APR
DT 01-APR
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DE NADH-1
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A., Wolstenholme D.R.;

Clary D.O., Wahleithner J.A., Wolstenholme D.R.;

"Sequence and arrangement of the genes for cytochrome b, URF1, URF4L, URF4, URF5, URF6 and five trNAs in Drosophila mitochondrial DNA.";

Nucleic Acids Res. 12:3747-3762(1984).

Nucleic Acids Res. 12:3747-3762(1984).
                                                                                                                                                                                         EMBL; X03240; CAA26994.1; ..

PIR; A30020; A30020.

FlyBase; FBgn0013186; Dyak\mt:ND4L.

InterPro; IPR001133; Oxidored_4L.

InterPro; IPR003214; Oxidred4L.
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SEQUENCE FROM N.A.

STRAIN-2317, 6 Ivory Coast;

MEDLINE-86089137; PubMed-3001325;

Clary D.O., Wolstenholme D.R.;

"The mitochondrial DNA molecular of Drosophila yakuba: nucleotide sequence, gene organization, and genetic code.";

J. Mol. Evol. 22:252-271(1985).
                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                               Oxidoreductase; NAD; Ubiquinone; Mitochondrion. SEQUENCE 96 AA; 11386 MW; 59ABEC7D738A174B CRC64;
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InterPro; IPR001133; Oxidored_4L.
InterPro; IPR003214; Oxidored4L.
Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 96 AA; 11359 MW; D383557D738A175B CRC64;
                                                                                                                                        Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1.
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01-APR-1988 (Rel. 07, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation updat
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EMBL;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Last annotation update)
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Mitochondrion.
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Matches 4; Conservative 0; Mismatches 0;

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Search completed: August 20, 2003, 12:34:53 Job time : 2.62918 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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# ALIGNMENTS

RESULT 1 AAY15748

AAY15748 standard; Peptide; 5

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AAY15748;

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Fluorogenic; fluorescent reporter molecule; enzyme substrate; apoptosis; protease; peptidase; apoptosis cascade; cancer; chemotherapeutic agent; cell death; viral protease activity.
                                                                                                                                                                                                                     Peptide used to make fluorescent reporter molecules
                                                                                                      09-OCT-1998;
                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                        27-JUL-1999 (first entry)
New fluorogenic or fluorescent reporter molecules
                    WPI; 1999-312448/26.
                                                                          03-MAR-1998;
10-OCT-1997;
                                                                                                                         22-APR-1999.
                                                                                                                                           WO9918856-A1.
                                                        (CYTO-) CYTOVIA INC.
                                     SX,
                                     Drewe JA, Keana JFW,
                                                                         98US-0033661.
97US-0061582.
                                                                                                     98WO-US21231.
                                       Weber
                                       (F)
                                       Zhang
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RESULT 2
AAX90902
ID AAX90902
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ID AAX90902
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) ZHANG H.
) CAI S X.
) DREWE J A.
) YANG W.
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                                                                                                                                                                                                                                                         Cai SX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      roup; halobenzoyl group; cleavage;
aminopeptidase type 2; MetAP-2; d:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ហ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0093642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US16423
                                                                                                                                                                                                                                                           Drewe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fluorescent label; fluorophore; rhodamine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease substrate peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                         JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20; DB
Pred. No. 9.3
); Mismatches
                                                                                                                                                                                                                                                         Yang
                                                                                            o acids or peptides, used as substrates modulators, e.g. anticancer or antivir. N-blocking group
                                                                                                                                                                                                                                                         Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.3e+05;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caspase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viral protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO:131
                                                                                                                    or antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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The invention

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activity of an

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involved ) be used volved in

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or measuring cascade in c

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109; 174pp;

English

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RESULT 3
AAY15739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC a halobenzoyl group on the fluorophore. They are of the structure CC peptide-Y-2, where Z represents a halo-substituted benzoyl blocking CC group, Y is a fluorescent or fluorigenic moiety (preferably a fluorescent or fluorigenic moiety (preferably a structure). The fluorescent or fluorigenic moiety (preferably a fluorescent or fluorigenic moiety (preferably a fluorescent or fluorigenic moiety) and the peptide-Y bond is cleavable by the enzyme being CC assayed. The labelled peptides are reporters for detecting intracellular proteally fluored in protection and the peptides and the enzymes involved in CC cytomegalovirus and hepatitis C virus proteases); and methionine CC cytomegalovirus and hepatitis C virus proteases); and methionine CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to identify modulators of these enzymes which may be potentially useful as agents for treating conditions such as cancer, neurodegeneration, CC autoimmune diseases, myocardial infarction and virla infection.

CC Modulators identified may also be used to prolong the life of cells being CC cultured for recombinant protein production, or to monitor the treatment of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are potential anti- angiogenic or anticancer agents. Sequences

CC ANYBOTRA-YBO910 represent peptides, some of which are specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
             substrate for enzymes involved in apoptosis or protease or peptidase enzymes. The compounds can be used as fluoregenic or fluorescent substrates for enzymes. Depending on the peptide molety used, the fluorescent molecules can be used for detecting or measuring the
                                                                      contain a peptide moiety (e.g. pre
substrate for enzymes involved in
                                                                                 AAY15618-Y15759 represent peptides used to make the fluorogenic fluorescent reporter molecules of the invention. These molecules contain a peptide molety (e.g. present sequence) which acts as a
                                                                                                                                                                                                       New
                                                                                                                                                                   Claim
                                                                                                                                                                                                                                         WPI; 1999-312448/26
                                                                                                                                                                                                                                                                                                                                                   03-MAR-1998;
10-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fluorogenic; fluorescent reporter molecule; enzyme substrate;
apoptosis; protease; peptidase; apoptosis cascade; cancer;
                                                                                                                                                                                                                                                                                                                 (CYTO-) CYTOVIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9918856-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemotherapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY15739 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      claimed, which may be used in assay methods according to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                 fluorogenic or fluorescent reporter molecules
                                                                                                                                                                 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                           Drewe JA,
                                                                                                                                                                 Page 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to make fluorescent reporter molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                   98US-0033661
97US-0061582
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                                                                                                                                                             202pp; English
                                                                                                                                                                                                                                                                             Keana
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                                                                                                                                                                                                                                                                             JFW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               se; apoptosis cascade; death; viral protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20;
Pred. No.
                                                                                                                                                                                                                                                                           Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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hes 0;
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                                                                                                                                                                                                                                                                         Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determine whether a test compound has an effect on an enzyme involved in the apoptosis cascade in cells; for determining the sensitivity of an animal with cancer to treatment with chemotherapeutic agents or determining whether a test substance inhibits, prevents, causes or enhances cell death of test cells; for detecting or measuring the activity of a viral protease in cells; for determining whether a test compound has an effect on the activity of a viral protease in cells; and for measuring the activity or determining whether a test substance
                    The invention relates to fluorescently labelled peptides containing a halobenzoyl group on the fluorophore. They are of the structure peptide-Y-2, where I represents a halo-substituted benzoyl blocking group, Y is a fluorescent or fluorigenic molety (preferably a rhodamine), and the peptide-Y bond is cleavable by the enzyme being assayed. The labelled peptides are reporters for detecting intracellular proteolytic enzymes, particularly caspases and other enzymes involved in apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human cytomegalovirus and hepatitis C virus proteases); and methionine aminopeptidase type 2 (MetAP-2). The peptides are particularly used to identify modulators of these enzymes which may be potentially useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZHAN/)
(CAIS/)
(DREW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protease substrate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY80893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY80893 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang
                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (YANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an effect on the activity of a protease or peptidase in
                                                                                                                                                                                                                                                                                                                                                                                                                             fluorescently labeled amino acids or peptides, used as detecting enzymes or their modulators, e.g. anticancer nts, contains a halobenzoyl N-blocking group \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOVIA INC. ZHANG H. CAI S X. DREWE J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YANG W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           group; halobenzoyl group; cleavage; caspase; vira
ne aminopeptidase type 2; MetAP-2; drug screening.
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                                                                                                                                                                                                                                                                                                                                                                              109; 174pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drewe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fluorescent label; fluorophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                              English.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yang
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9.3e+05;
ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rhodamine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID NO:122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              viral protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    substrates
or antiviral
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Matches 4
Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases, myocardial infarction and virla infection.

Modulators identified may also be used to prolong the life of cells being cultured for recombinant protein production, or to monitor the treatment of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are potential anti- angiogenic or anticancer agents. Sequences AAY80782-Y80910 represent peptides, some of which are specifically claimed, which may be used in assay methods according to the invention.
                                                                                                                    The present invention relates to a culture method for propagating a plant from a plant starting material, where root or shoot initiation is stimulated by introducing a gene into the starting material which allows the reduction or absence of phytochrome addition to the culture. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vegetative propagation; RKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A thaliana receptor kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO17262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAO17262 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                 method is used for the propagation (preferably, seedless propagation) of a plant from a plant starting material in an in vitro culture method. Nucleic acids encoding receptor-like kinases are useful in the method.
                                                                                                                                                                                                     recombinant phytochrome
                                                                                                                                                                                                       In vitro culture propagation of a plant from plant starting material, comprises stimulating root/shoot initiation by introducing a recombinant gene product into the starting material, thus reducing phytochrome addition to culture
                                                                                                                                                                                                                                                                                                                                                                                                             EP1094113-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                Sequence
                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                (GENE-) GENETWISTER TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                         22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2001
                                                                        present sequence
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milarity 100.
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                08;
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                                                                         fragment of a receptor-like kinase
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                                   ABR44913;
                                                                                                           ABR44913 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation; cardiovascular disease; central nervous system disease gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nontransistantical informations of the property of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 11; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JARI-) JARI PHARM BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUN-2003
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Strijp JAG;
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                                                                                                           Peptide;
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entral nervous system disease;
genitourinary disease;

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Best Local
         CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease;
                                                                          Staphylococcus aureus CHIPS-related peptide #491
                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to peptides (ABR44811-ABR47162 and ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include
                                                                                                            10-JUN-2003
                                                                                                                                           ABR45301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Combination of peptides derived from chemotaxis inhibiting protein from Staphlylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases
                                                                                                                                                                     ABR45301 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Van Strijp JAG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus CHIPS-related peptide #103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lifiammation; cardiovascular disease; central nervous system disease
gastrointestinal disease; skin disease; genitourinary disease;
joint disease; respiratory disease; HIV infection; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUN-2003
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RESULT 9
ABR4501
ID ABR4
XX ABR4
XX ABR4
XX ABR4
XX CHII
KW CHII
KW Forn
KW Infl
KW Joli
KW Joli
KW Gyn
XX Stag
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      joint disease; respiratory disease; HIV infection; antiinflammatory;
cardiant; cerebroprotective; neuroprotective; nootropic; dermatologi
gynecological; immunosuppressive; anti-HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Combination of peptides derived from chemotaxis inhibiting protein Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
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                                                                                       CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 12; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JARI-) JARI PHARM BV
                                                                                                                                                                                               Staphylococcus aureus CHIPS-related peptide #495.
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                                                                                                                                                                                                                                                                                        ABR45305 standard;
                                                                         gynecological;
                                              Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kessel CPM,
Strijp JAG;
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4; Conserv
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ilarity 100.0%;
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                                                                                                                                                                                                                               (first entry)
                                              aureus
                                                                         1mmunosuppressive;
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                                                                                                                                                                                                                                                                                        Peptide;
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9.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 6;
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XX 10-JU
XX Staph
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DE Staph
CHIPS
KW CHIPS
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Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Combination of peptides derived from chemotaxis inhibiting protein Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and
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                                                                                                                                                                                                                         formylated peptide receptor; FPR; neutrophil; monocyte; endothelial inflammation; cardiovascular disease; central nervous system disease gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                   Synthetic
                                                                                                                                                                Staphylococcus
                                                                                                                                                                                              gynecological;
                                                                                                                                                                                                                                                                                        CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus CHIPS-related peptide #827.
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                                                                                           23-JAN-2003
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Strijp JAG;
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                                                                                                                                                                    aureus.
                                                                                                                                                                                                 immunosuppressive;
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                                                                                                                                                                                                                 neuroprotective; nootropic;
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11-JUL-2001; 11-JUL-2001;

2001WO-EP08004 2001WO-EP08004

cell;

(JARI-) JARI PHARM BV

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RESULT 11
ABR45641
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Matches
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Combination of peptides derived from chemotaxis inhibiting protein Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
                                                                                                                                                                                                                                       11-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endoth inflammation; cardiovascular disease; central nervous system d gastrointestinal disease; skin disease; genitourinary disease; seriorinary di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, central diseases,
                                                                                                                                                                                                                                                                                                                                  23-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus
                                                                                                                                                                                            (JARI-) JARI PHARM
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                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gynecological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus CHIPS-related peptide #831.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 13; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to peptides (ABR44811-ABR47162 and ABR47164 ABR47385) derived from the Chemotaxis Inhibitory Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oint disease;
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                                                                                                                         Kessel CPM,
Strijp JAG;
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Strijp JAG;
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                                                                                                                                             Gosselaar-de
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                                                                                                                                             CJC,
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. 9.3e+05;
ches 0;
                                                                                                                                          Kruijtzer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatological;
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The present invention relates to peptides (ABR44811-ABR47162 and ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein from Staphylococcus aureus. The peptide fragments are useful in

Protein

(CHIPS)

Disclosure;

Page

English.

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RESULT 12
ABR46029
ID ABR46
XX CHIP
XX CHIP
XX GAT
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                                                                                                                                                                            Staphylococcus prophylaxis and
                                                                                                                                                                                                                                Combination of
                                                                                                                                                                                                                                                                                                                                                                                                          (JARI-) JARI PHARM BV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003006048-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gynecological; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestinal disease; skin disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus CHIPS-related peptide #1219.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR46029 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR46029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    joint disease; respiratory disease; HIV infection; antiin
pardiant; cerebroprotective; neuroprotective; nootropic;
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kidney diseases
                                                                                                                                                                                                                                                                                                                              Kessel CPM,
Strijp JAG;
                                                                                                                                                                                                                                                                                  2003-247783/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemotaxis Inhibitory Protein; C5a-receptor;
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4; Conservative
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                                                                                                                                                                    peptides derived from chemotaxis inhibiting protein from aureus (CHIPS) having CHIPS activity, useful in d treatment of infiammation, cardiovascular, skin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aureus
                                                                                                15; 89pp;
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                                                                                                                                                                                                                                                                                                                                                         Gosselaar-de
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HIV infection; antlinflar
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ches 0;
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Matches 4
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                           The present invention relates to peptides (ABR44811-ABR47162 and ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial celis or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint gastrointestinal diseases, skin diseases, genitourinary diseases, joint
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            formylated peptide receptor; FPR; neutrophil; monocyte; endothelial c inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory;
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gynecological; immunosuppressive; anti-HIV.
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RESULT 14
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                                                                                The present invention relates to peptides (ABR44811-ABR47162 and ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein is from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothellal cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, diseases, respiratory diseases and HIV infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                  The present invention relates to peptides (ABR44811-ABR47162 and ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (C from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, jc diseases, respiratory diseases and HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Kessel CPM, Gosselaar-de Haas CJC,
Van Strijp JAG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 16; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kidney diseases
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SFSF 5
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Mismatches 0;
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Search completed: August 20, 2003, 12:33:43 Job time: 9.79518 secs

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Result
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Maximum DB
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   protein search, using sw
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2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/1aa/backfiles1.pep:*
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US-09-521-650-122
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US-09-521-650-33
US-09-521-650-33
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US-09-688-33
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US-09-688-33
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US-08-630-915A-187
US-08-630-915A-202
US-08-630-915A-202
US-09-230-2258-13
US-09-230-2258-13
US-09-230-2258-13
US-09-230-258-882
US-09-231-257-624
US-09-231-257-624
US-09-231-257-624
US-09-231-257-634
US-09-231-257-634
US-09-215-221-16
US-09-149-476-619
US-09-205-258-431
US-09-205-258-431
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33, Appl
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11, Appl
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20, Appl
20, Appl
16, Appl
15, Appl
16, Appl
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US-09-357-952-131
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4832, Ap	13, Appl	9, Appli	4962, Ap	262, App	1246, Ap	5775, Ap	294, App		7435, Ap	5188, Ap	29, Appl	367, App	•	25, Appl		25, Appl	25, Appl

### ALIGNMENTS

GENERAL INFORMATION: Patent No. 6248904

for Who

Application US/09357952

```
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Yang, Wu
APPLICANTON: O. 6248904el Fluorescence Dyes and Their Applications for V
ITILE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735.0030001
CURRENT APPLICATION NUMBER: US/09/357,952
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER FILING DATE: 21-UI-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic ; OTHER INFORMATION: Peptide US-09-357-952-131
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Best Local S
Matches 4
                                                                                                                                                                                              Sequence 131, Application US/09521650 Patent No. 6335429 GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John A.
APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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OF INVENTION: Use Thereof

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APPLICANT: Chee, John F.W.

APPLICANT: Drewe, John A.

APPLICANT: Drewe, John A.

APPLICANT: Drewe, John A.

APPLICANT: Drewe, John A.

APPLICANT: Zhang, Han-Zhong

ITILE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and

TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

TITLE OF INVENTION: Use Thereof

FILE REFERENCE: 1735.029002

CURRENT APPLICATION NUMBER: US/09/168,888

CURRENT FILING DATE: 1998-10-99

EARLIER APPLICATION NUMBER: US 00/061,582

EARLIER APPLICATION NUMBER: US 09/033,661

EARLIER APPLICATION DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 142

SOSTWARE: Patentin Ver. 2.0
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RESULT 4
US-09-357-952-122
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CURRENT APPLICATION NUMBER: US/09/521,650
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 09/168,888
EARLIER FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER FILING DATE: 1997-10-10
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
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                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Pred. No.
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CURRENT FILING DATE: 1999-07-21

EARLIER APPLICATION NUMBER: US/09/357,952

EARLIER APPLICATION NUMBER: US/09/3542

EARLIER FILING DATE: 21-JUL-1998

NUMBER OF SEQ ID NOS: 139

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 139
                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 122
LENGTH: 6
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/521,650
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 09/168,888
EARLIER FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER APPLICATION NUMBER: US 09/033,661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and TITLE OF INVENTION: Use Thereof FILE REFERENCE: 1735.0290002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Weber, Eckard APPLICANT: Cai, Sui Xiong
                                                                                                                                                                                                                                                                      EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
                                                                                         OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                    TYPE: PRT
                                                                                                                                        FEATURE:
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No. 6248904
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                                                                                      Description of Artificial Sequence:Synthetic Peptide
100.0%;
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Score 20; DB 4;
Pred. No. 2.5e+05;
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Pred. No.
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                  Length 6;
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APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
APPLICANT: Chang, Han-Zhong
TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: USe Thereof
FILE REFERENCE: 1735.0290002
CURRENT APPLICATION NUMBER: US6/061,588
CURRENT FILING DATE: 1998-10-99
EARLIER APPLICATION NUMBER: US 60/061,582
EEARLIER APPLICATION NUMBER: US 09/033,661
EARLIER APPLICATION DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
COMMADER: USC 1998-03-03
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US-09-168-888-122
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic; OTHER INFORMATION: Peptide US-09-357-952-33
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SEQ ID NO 122
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                                                                                                                                                                                     APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
APPLICANT: Yang, Wu
APPLICANT: Yang, Wu
TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications f
TITLE OF INVENTION: Other Enzymes and the Use Thereof
TITLE REFERENCE: 1735.0030001
CURRENT FILING DATE: 1939-07-21
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEO ID NOS: 139
NUMBER OF SEO ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                        FEATURE:
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llarity 100.0%;
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Pred. No. 2.5e+05;
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US-09-521-650-33
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LENGTH: 7
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Best Local Similarity
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Patent No. 6342611
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APPLICANT: Cal. Sul Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Ekena, John A.
APPLICANT: Lrewe, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules
TITLE OF INVENTION: Screening Assays for Whole-Cell Fluorescence
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.0290002
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APPLICANT: Weber, Eckard
APPLICANT: Cal, Sul Xiong
APPLICANT: Cal, Sul Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
APPLICANT: Drewe, John A.
APPLICANT: Drewe, John A.
TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules
TITLE OF INVENTION: Screening Assays for Whole-Cell Fluorescence
TITLE OF INVENTION: Use Thereof
FILE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.029002
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER FILING DATE: 1997-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/521,650 CURRENT FILING DATE: 2000-03-08 EARLIER APPLICATION NUMBER: 09/168,888 EARLIER FILING DATE: 1998-10-09 EARLIER APPLICATION NUMBER: US 60/061,582 EARLIER FILING DATE: 1997-10-10 EARLIER APPLICATION NUMBER: US 09/033,661
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SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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Pred. No.
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Pred. No. 2.5e+05;
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US-09-817-413-19
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US-09-053-941-19
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                                                                                                                                                                                     Sequence 19, Application US/09817413 Patent No. 6436648 GENERAL INFORMATION:
                  SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                          CURRENT APPLICATION NUMBER: US/09/817,413
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/043,380
PRIOR FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 25
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                                                                                                                     APPLICANT: SRINIVISAN, ALGARSAMY
APPLICANT: KOPROWSKI, HILARY
TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
FILE REFERENCE: Chimeric Viral Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human immunodeficiency virus type 1 PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 25
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NUMBER OF SEQ ID NOS: 142
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VOLUME: 38
PAGES: 299-
DATE: 1974
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TYPE: PRT
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OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
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ENGTH: 10
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Pred. No.
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                                                        Matches
                                                                    Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION:
JOURNAL: Meth. Enzymol.
VOLUME: 38
PAGES: 299-
DATE: 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MOORE
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                   TELEFAX: (516) 822-358 INFORMATION FOR SEQ ID NO:
                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pept
                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: O'Dea, Sean W.
REGISTRATION NUMBER: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 822-3550
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/8 FILING DATE: March 28, 1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM CONTROL OPERATING SYSTEM: SOFTWARE: WORDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 350 Je
CITY: Jericho
STATE: New You
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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                         1 SFSF 4
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                                                                    Similarity
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                                                                                                                                                                                                                                                                           37690
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Pred. No.
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Pred. No.
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RESULT 13 US-08-630-915A-187 ; Sequence 187, Application ; Patent No. 6309820

GENERAL INFORMATION: APPLICANT: SPARKS

SPARKS,

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Best Local Similarity
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NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 1872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                         tent No.
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TITLE OF INVENTION:
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TITLE OF INVENTION:
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                COMPUTER READABLE FORM:
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                                                              CITY: New York
STATE: New Yor
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                                 COUNTRY: USA
ZIP: 10036-2711
                                                                                              STREET:
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                                                              New York
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1155 Avenue of the Americas
                                                                                              E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                          Application US/08630915A
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(212) 869-8864/9741
                                                                                                                                                                         MCCONNELL, Stephen J.

VENTION: POLYPEPTIDES HAVING A FUNCTIONAL

VENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                          KAY, Brian K. FOWLKES, Dana M.
                                                                                                                                                                                                                                                        HOFFMAN, No. 6309820h
                                                                                                                                                                                                                                                                         SPARKS, Andrew B
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N: 536
Floppy disk
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: 227
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227
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Pred. No.
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US-08-825-369A-2
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Patent No. 6084060
GENERAL INFORMATION:
APPLICANT: Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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                             TELEFAX: (516) 822-3582 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 790-9090
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                                                           REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: O'Dea, Sean W.
REGISTRATION NUMBER: 37690
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                      SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
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             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES
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OTHER INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                      APPLICATION NUMBER: US/08/6 FILING DATE: March 28, 1997 CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                     COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS
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ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOSITION AND METHOD FOR PRESERVING PROGENITOR CELLS
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                  & Baron, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18,872
                                                                                                                                                                                                                                                                     3.50 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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                                                                                              381-21 CIP
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Page 6

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Search completed: August 20, 2003, 12:44:20 Job time: 4.77108 secs
                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-825-369A-2
                                                                                                                         Query Match 100.0%; Score 20; DB 3; Length 14; Best Local Similarity 100.0%; Pred. No. 55; Matches 4; Conservative 0; Mismatches 0; Indels
                                                               1 SFSF 4
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5 SFSF 8
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Title:
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Maximum Match 100%
Listing first 45 summaries
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No.
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Maximum DB
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/Pi
2: /cgn2_6/ptodata/1/pubpaa/Pi
3: /cgn2_6/ptodata/1/pubpaa/Pi
4: /cgn2_6/ptodata/1/pubpaa/Pi
6: /cgn2_6/ptodata/1/pubpaa/Pi
6: /cgn2_6/ptodata/1/pubpaa/Pi
7: /cgn2_6/ptodata/1/pubpaa/Pi
7: /cgn2_6/ptodata/1/pubpaa/Ui
8: /cgn2_6/ptodata/1/pubpaa/Ui
9: /cgn2_6/ptodata/1/pubpaa/Ui
10: /cgn2_6/ptodata/1/pubpaa/Ii
11: /cgn2_6/ptodata/1/pubpaa/Ii
13: /cgn2_6/ptodata/1/pubpaa/Ii
14: /cgn2_6/ptodata/1/pubpaa/Ii
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/cgn2_6/ptcdata/1/pubpaa/US09A_PUBCOMB.pep:*
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Sequence 30, Appl
Sequence 131, App
Sequence 132, Appl
Sequence 33, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 202, Appl
Sequence 202, Appl
Sequence 46, Appl
Sequence 413, Appl
Sequence 413, Appl
Sequence 3, Appli
Sequence 158, Appl
Sequence 158, Appli
Sequence 158, Appli
Sequence 345, Appli
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16,	Sequence 14, Appl	306, 1	151,	4492	25	2	Sequence 874, App	Sequence 42675, A	768	Sequence 431, App	Sequence 34120, A	850,	850,	Sequence 143, App	Sequence 10, Appl	e 450,					7459	e 670,	~		e 882,	~	Sequence 624, App	e 142,	Sequence 44483, A

#### ALIGNMENTS

US-09-300-425B-30

GENERAL INFORMATION:

APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred

Sequence 30, Application US/09300425B Publication No. US20030045681A1

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PRIOR APPLICATION NUMBER: 09/07
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 4
TYPE: PRT
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Matches 4
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                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B OTHER INFORMATION: antibody clone
                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                              FEATURE:
                                    1 SFSF 4
                                                                                              Similarity
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
                                                                          100.0%; Score 20; D:
100.0%; Pred. No. 4.
tive 0; Mismatches
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                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 122
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Best Local
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                                                                                                                                                       NUMBER OF SEQ ID NOS: 142
                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/145,746 PRIOR FILING DATE: 1998-03-03 PRIOR APPLICATION NUMBER: US 09/168,888 PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/947,387 CURRENT FILING DATE: 2001-09-07 PRIOR APPLICATION NUMBER: US 60/061,582 PRIOR FILING DATE: 1997-10-10 PRIOR APPLICATION NUMBER: US 60/145,746 PRIOR APPLICATION NUMBER: US 09/168,888 PRIOR APPLICATION NUMBER: US 09/168,888
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Their Applications
TITLE OF INVENTION: Screening Assays for
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.0290005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui xiong
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/947,387
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TITLE OF INVENTION: Use The
FILE REFERENCE: 1735.0290005
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APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: NO. US20020150885Alel Fluorogenic or Fluorescent Reporter Molecu.
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecu
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
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NUMBER OF SEQ ID NOS: 142
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                                                                                             ENGTH:
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                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/061,582 FILING DATE: 1997-10-10
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D. US20020150885A1
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Drewe, John A.
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US-09-205-658-293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                  EARLIER APPLICATION NUMBER: 08/857,076
EARLIER FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: 08/888,534
EARLIER FILING DATE: 1997-07-07
                                                                                                                                                TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE FILE REFERENCE: 00786/351004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/947,387
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/061,582
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1998-03-03
                                                                                                                                                                                                                 APPLICANT: Ruvkun, Gary APPLICANT: Ogg, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/168,888 PRIOR FILING DATE: 1998-10-09
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NUMBER OF SEQ ID NOS: 142
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TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
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APPLICANT: Cai, Sui Xiong
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                                                                                                     APPLICATION NUMBER: US/09/205,658 FILING DATE: 1998-12-03
APPLICATION NUMBER: US98/10080
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Drewe, John A.
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TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: peptide chain of pylartin protein US-09-934-251A-1
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US-09-879-957-187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09934251A Patent No. US20020132017A1 GENERAL INFORMATION:
APPLICANT: MOOIE, Jeffrey G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 328
'SOFTWARE: FastSEQ for Windows Version SEQ ID NO 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                              Sequence 187, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Composition and Method for Preserving Progenitor Cells FILE REFERENCE: 108236.136
CURRENT APPLICATION NUMBER: US/09/934,251A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/368,607
PRIOR PILING DATE: 1999-08-05
PRIOR PILING DATE: 1999-08-05
PRIOR FILING DATE: 1996-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                              TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                        NUMBER OF SEQUENCES: 227
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                                                                    CITY: New York
STATE: New York
                                                         COUNTRY:
                                                                                                                                                                                                                                               KAY, Brian K.
FOWLKES, Dana M.
                                                                                                                                                                                                                                MCCONNELL,
                                                         USA
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Pred. No. 1.
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Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 187:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
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                   APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                               APPLICATION NUMBER: US/09/879,957
ETLING DATE: 13-Jun-2001
CLASSIETICATION: c/unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown MOLECULE TYPE: peptide
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                STATE: New York
                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 20; DB 9; ilarity 100.0%; Pred. No. 1.4e+02. Conservative 0; Mismatches 0.
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HOFFMAN, No. US20020034755Alh
KAY, Brian K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAY, Brian K.
FOWLKES, Dana M.
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 790-9090
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US-09-775-052-46
; Sequence 46, Application US/09775052
; Publication No. US20030054000A1
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                                                                                                                      GENERAL INFORMATION:
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Patent No. US20020132017A1
GENERAL INFORMATION:
APPLICANT: Moore, Jeffrey G.
TITLE OF INVENTION: Composition and Method for Preserving Progenitor Cells
FILE REFERENCE: 108236.136
CURRENT APPLICATION NUMBER: US/09/934,251A
CURRENT FILING DATE: 2001-08-21
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 14
TYPE: PRI
ORGANISM: Artificial Sequence
CURRENT APPLICATION NUMBER: US/09/775,052
CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 09/208,966
PRIOR FILING DATE: 1998-12-10
                                                               APPLICANT: Dowdy, Steven F.
TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS
FILE REFERENCE: 48881/1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: US 08/762,537
PRIOR FILING DATE: 1996-12-09
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No.
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thes 0;
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                                                                                 OF USE THEREOF
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Query Match
Best Local Similarity
Whethes 4; Conserve
                               PRIOR APPLICATION NUMBER: 09/892,877
PRIOR FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: 09/437,658
PRIOR APPLICATION NUMBER: PCT/US99/09847
PRIOR APPLICATION NUMBER: PCT/US99/09847
PRIOR FILING DATE: 1999-05-06
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens US-09-892-877-413
                                                                                                                                                                                                                                                                                                                                                                       US-09-948-783-413
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US-09-892-877-413
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                                                                                                                                                                                                                                                                                                               Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Sequence 413,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 413
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 413, Application US/09892877 Publication No. US20030077809A1
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Best Local Similarity
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                                                                                                                                                                                CURRENT FILING DATE: 2001-09-10 PRIOR APPLICATION NUMBER: 60/231,846 PRIOR FILING DATE: 2000-09-11
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/948,783
CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                        APPLICANT: Ruben et. al.
TITLE OF INVENTION: 97 Human secreted proteins
FILE REFERENCE: PZ028P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ruben et. al. TITLE OF INVENTION: 97 Human secreted proteins FILE REFERENCE: PZ028P1
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ORGANISM: human
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FILING DATE: 1998-05-
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NUMBER: 60/085,105

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1998-05-1 1998-05-1998-05-12

60/085,906 60/085,927 60/085,180

FILING DATE: 1998-05-18

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PRIOR APPLICATION NUMBER: PCT/EP01/01549
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 25
SOSTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 22
TYPE: PRT
ORGANISM: Coffee arabica
US-10-260-212-3
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RESULT 14
US-09-983-802-158
; Sequence 158, Application US/09983802
; Publication No. US20030022185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
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Best Local Similarity
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; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 345
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-065-345
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PRIOR APPLICATION NUMBER: PCT/US98/27059
PRIOR FILING DATE: 1998-12-17
PRIOR PPLICATION NUMBER: PCT/US98/27059
PRIOR FILING DATE: 1997-12-18
PRIOR PPLICATION NUMBER: 60/068,007
PRIOR FILING DATE: 1997-12-18
PRIOR PPLICATION NUMBER: 60/068,007
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,006
PRIOR APPLICATION NUMBER: 60/068,369
PRIOR APPLICATION NUMBER: 60/068,369
PRIOR PILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR PILING DATE: 1997-12-19
PRIOR PILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,068
PRIOR PILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,053
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,064
PRIOR PILING DATE: 1997-12-18
PRIOR PILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,064
PRIOR PILING DATE: 1997-12-18
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US-10-097-065-345
; Sequence 345, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
APPLICANT: MOORE, Paul A. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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, NAME/KEY: SITE
; LOCATION: (23)
; OTHER INFORMATION: Xaa equals stop translation
US-09-983-802-158
                                                                                                                     Matches 4; Conservative
                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 158
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/068,365 PRIOR FILING DATE: 1997-12-19
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TITLE OF INVENTION: 110 Human Secreted Proteins
TLE REFERENCE: PZ021P1
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TYPE: PRT
ORGANISM: Homo sapiens
11, SFSF 14
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17 SFSF 20
                                                             1 SFSF 4
                                                                                                         100.0%; Score 20; DB 15;
100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0;
                                                                                                                                                                 Length 23;
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Search completed: August 20, 2003, 13:16:46 Job time : 5.33735 secs

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Title:
Perfect score:
Sequence:
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Maximum DB seq
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                                                                                                                                                                                     Pred. No.
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                                                                                                                                            No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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Match
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./Gyn2_6/ptodata/1/paa/US06_COMB.pep:*
./Gyn2_6/ptodata/1/paa/US07_COMB.pep:*
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Listing first 45 summaries
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 US-09-075-338C-30
US-09-300-425B-30
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 Sequence 30, 
Sequence 30,
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US-09-075-338C-30
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Sequence Sequence Sequence Sequence Sequence	equence 46, Apequence 46, Apequence 45, Apequence 4572, equence 6522, equence 12693, equence 6522, equence 6522, equence 6522, equence 6523, equence 12693, Apequence 12693, Apequence 293, Apequence 2626, Appquence 293, Appqu	Sequence 12 Sequence 13 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 6 Sequence 7	quence 131, P

## ALIGNMENTS

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RESULT 1
US-09-075-338C-30

(Sequence 30, Application US/09075338C

Sequence 30, Application US/09075338C

(SENERAL INFORMATION:

APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: TARLI, Lorenzo
APPLICANT: BIRCHLER, Manifred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
FILE REFERENCE: SCH-1733
CURRENT FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B
OTHER INFORMATION: antibody clone
US-09-075-338C-30

Query Match
Best Local Similarity 100.0%; Pred. No. 5.2e+06;
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US-09-512-082-30
                                                                                                                               PRIOR FILING DATE: 19:
NUMBER OF SEQ ID NOS:
SOFTWARE: PATENTIN VE:
SEQ ID NO 30
LENGTH: 4
TYPE: PRT
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     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
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                                                                                                                                                                                                                           CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 09/300,425
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGIOGENESIS FILE REFERENCE: SCH-1733P2
CURRENT APPLICATION NUMBER: US/09/512,082
CURRENT FILING DATE: 2000-02-24
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APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/300,425B CURRENT FILING DATE: 199-04-28 PRIOR APPLICATION NUMBER: 09/075,338 PRIOR FILING DATE: 1998-05-11 NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
                                                        OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
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                                                        Description of Artificial Sequence: anti-ED-B antibody clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; 100.0%; Pred. No. tive 0; Mismatch
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 Score
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; FEATURE:
; OTHER INFORMATION:
; OTHER INFORMATION:
PCT-US99-16423-131
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Best Local Similarity
Yatches 4; Conserve
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      Query Match
                                                                                                                                                                               SEQ ID NO 131
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                                                                                                                                                                                                         APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
APPLICANT: Yang, Wu
APPLICANT: Yang, Wu
ITITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications for Whole-Cell
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protea
FILE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735.0039C01
CURRENT APPLICATION NUMBER: PCT/US99/16423
CURRENT APPLICATION NUMBER: US 60/093,642
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
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APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
                                                                                                      LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                 SOFTWARE: PatentIn Ver.
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TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
FILE REFERENCE: 1735.0399C02
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EARLIER FILING DATE: 1997-10-10
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OTHER INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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ilarity 100.0%;
Conservative (
                                                            Description of Artificial Sequence:Synthetic Peptide
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      100.0%;
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Pred. No. 5.2
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ches 0;
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APPLICANT: Keans, John F.W.
APPLICANT: Drawe, John A.
APPLICANT: Drawe, John A.
APPLICANT: Drawe, John A.
APPLICANT: Drawe, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: Screening Assays for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.0290005
CURRENT APPLICATION NUMBER: US/09/947,387
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/061,582
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: US 09/168,888
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                                                                  PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 131
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Best Local Similarity
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CURRENT FILING DATE: 2000-05-30
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APPLICANT: Cai, Sui xiong
APPLICANT: Drewe, John A.
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PRIOR FILING DATE: 21-JUL-1999
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
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equence 131, Application US/09947387
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TYPE: PRT
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APPLICANT: Yang, Wu
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APPLICANT: Cai, Sui Xiong
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ORGANISM: Artificial Sequence
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nilarity 100.0%;
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); Mismatches 0;
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Pred. No. 5.2e+06;
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US-10-138-375-131
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                                                      SOFTWARE: PatentIn Ver.
SEQ ID NO 122
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                                                                                          APPLICANT: Cytovia, Inc.
TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.02pc02
CURRENT APPLICATION NUMBER: PCT/US98/21231
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER FILING DATE: 1997-10-10
EARLIER TILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
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CURRENT FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642

PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998

NUMBER OF SEQ ID NOS: 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Drewe, Jo
APPLICANT: Yang, Wu
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TYPE: PRT
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                  TYPE: PRT
ORGANISM: Artificial Sequence
                                     ENGTH:
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Drewe, John A.
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Pred. No.
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Pred. No.
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; OTHER INFORMATION:
PCT-US98-21231-122
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                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 122
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local
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APPLICANT:
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Best Local 9
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APPLICANT: Zhang, Ham -
APPLICANT: Cai, Sui Xiong
Prewe, John A.
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                                                                                                                                     TITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications for Whole-Cell TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, ProteTITLE OF INVENTION: Other Enzymes and the Use Thereof FILE REFERENCE: 1735.003001

CURRENT APPLICATION NUMBER: US/09/583,225

CURRENT FILING DATE: 2000-05-30
                                                                                  PRIOR APPLICATION NUMBER: 09/357,952
PRIOR FILING DATE: 21-JUL-1999
NUMBER OF SEQ ID NOS: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications for Whole-Cell TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protein TITLE OF INVENTION: Other Enzymes and the Use Thereof FILE REFERENCE: 1735,003pc01
CURRENT APPLICATION NUMBER: PCT/US99/16423
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cytovia, Inc.
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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                                      ENGTH:
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Yang, Wu
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RESULT 13
US-10-138-375-122
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US-09-583-225-122
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Best Local :
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SEQ ID NO 122
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CURRENT APPLICATION NUMBER: US/10/138,375
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
                                                                                                         TITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, PeTITLE OF INVENTION: Other Enzymes and the Use Thereof FILE REFERENCE: 1735.0030001
                                                                                                                                                                                              APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
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APPLICANT: Drewe, John A.

APPLICANT: Drewe, John A.

APPLICANT: Lang, Han-Ehong

TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and

TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence

TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

TITLE OF INVENTION: Use Thereof

TITLE REFERENCE: 1735.0290005
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CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/061,582
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1998-03-03
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5.2e+06;
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; OTHER INFORMATION: Description of Artificial Sequence:Synthetic; OTHER INFORMATION: Peptide US-10-138-375-122
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; OTHER INFORMATION: Description of Artificial Sequence:Synthetic; OTHER INFORMATION: Peptide
pcT-us98-21231-33
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PCT-US99-16423-33
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Best Local Similarity 100.08;
Matches 4; Conservative
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GENERAL INFORMATION:
APPLICANT: Cytovia, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the TITLE OF INVENTION: Use Thereof FILE REFERENCE: 1735.029PC02

CURRENT APPLICATION NUMBER: PCT/US98/21231

CURRENT FILING DATE: 1998-10-09

EARLIER APPLICATION NUMBER: US 60/061,582

EARLIER FILING DATE: 1997-10-10

EARLIER FILING DATE: 1998-03-03

ROTHUMBER: US 09/033,661

EARLIER FILING DATE: 1998-03-03

RUMBER OF SEQ ID NOS: 142

ROTHUMBER: US DESCRIPTOR OF SEQ ID NOS: 142

ROTHUMBER: DESCRIPTOR OF SEQ ID NOS: 142
                                                                                                                                                                                                                                                                      Sequence 33, Application PC/TUS9916423 GENERAL INFORMATION:
                                                          APPLICANT: Cytovia, Inc.
APPLICANT: Chang, Han-Thong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.

APPLICANT: Yang, Wu
TITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications for Whole-Cell
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protes
TITLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735.003PC01
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
EARLIER APPLICATION NUMBER: US 60/093,642
                CURRENT APPLICATION NUMBER: PCT/US99/16423
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Search completed: August 20, 2003, 13:13:40 Job time : 41.9398 secs
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                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
PCT-US99-16423-33
                                                                                                                                                                                                                                                 EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 33
                                                                                                       Matches
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ORGANISM: Artificial Sequence
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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3326, Ap
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234078, A
224077, A
2240772, A
25621, App
2151, App
2152, App
21539, A
26647, A
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US-10-603-113-24061	US-10-603-113-25632	US-10-603-113-24293	US-10-603-113-21184	US-10-631-441-1780	US-10-631-402-1780	US-10-603-113-26215	US-10-603-113-24912	US-10-617-320-4732	US-10-603-113-27444	US-10-603-113-21888	US-10-612-783-5219	US-10-603-113-25759	US-10-603-113-23802	US-10-617-320-4664	US-10-273-573-8204	US-10-603-113-25419	US-10-603-113-22184	US-10-291-265-902	
Sequence 24061	Sequence 25632	Sequence 24293	Sequence 21184	Sequence 1780	Sequence 1780,	Sequence 26215	Sequence 24912	Sequence 4732,	Sequence 27444	Sequence 21888	Sequence 5219,	Sequence 25759	Sequence 23802	Sequence 4664	Sequence 8204,	Sequence 25419	Sequence 2218	Sequence 902,	
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### ALIGNMENTS

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RESULT 1
US-09-63-693A-293
I Sequence 203, Application US/09963693A
GENERAL INFORMATION:
APPLICANT: RAVKIN, GAIY
APPLICANT: LINEOWANTON: THERAPBUTIC AND DIAGNOSTIC TOOLS FOR TITLE OF INVENTION: THERAPBUTIC AND DIAGNOSTIC TOOLS FOR TITLE OF INVENTION NUMBER: US/09/63,693A
CURRENT APPLICATION NUMBER: US/09/63,693A
CURRENT APPLICATION NUMBER: US/09/63,693A
CURRENT APPLICATION NUMBER: US/09/63,693A
PRIOR APPLICATION NUMBER: US/09/63,693A
PRIOR APPLICATION NUMBER: US/09/63,693A
PRIOR APPLICATION NUMBER: US/09/63,693A
PRIOR APPLICANT ON THE US/10389674
GENERAL INFORMATION: INFORMATION: THE ALPHA HOMOLOGUES
FILE REFERENCE: 02-101510/0140,002
CURRENT APPLICANTON NUMBER: US/09/685,189
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                                                                                                                                                                                                                                                                                          Sequence 3325, Application US/10631402 GENERAL INFORMATION:
                                           PRIOR APPLICATION NUMBER: US 08/905,223
PRIOR TILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,135
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR APPLICATION NUMBER: US 08/905,051
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Best Local :
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LENGTH: 52
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                                                                                                                                                                      TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins FILE REFERENCE: GEN-1119C1
CURRENT APPLICATION NUMBER: US/10/631,402
CURRENT FILING DATE: 2003-07-30
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                                                                                                                                  PRIOR APPLICATION NUMBER: US/09/547,599C PRIOR FILING DATE: 2000-04-11
                                                                                                                                                                                                                                                                       APPLICANT: Dumas Milne Edwards, Jean Baptiste
                                                                                                                                                                                                                                             APPLICANT:
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NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/368,433A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GICQUEL, BRIGITTE
TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM TUBERCULOSIS
FILE REFERENCE: 05394.0009-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: JACKSON, MARY APPLICANT: GICQUEL, BRI
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TYPE: PRT
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PRIOR FILING DATE: 1996-07-26
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TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICATION NUMBER: US 08/905,144 FILING DATE: 1997-08-01
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CURRENT FILING DATE: 2003-07-30
NUMBER
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                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/547,5990
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dumas Milne Edwards, Jean Baptiste
                                                                                                                                                                                                                                                                                                                                                                       !ITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
!ILE REFERENCE: GEN-T119C1
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EQ ID NO 3325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 08/905,133
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OTHER INFORMATION:
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OTHER INFORMATION:
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           APPLICATION NUMBER: US 08/905,133 FILING DATE: 1997-08-01
                                                APPLICATION NUMBER: US FILING DATE: 1997-08-01
                                                             FILING DATE: 1997-08-01
APPLICATION NUMBER: US 08/905,134
                                                                                                                                    APPLICATION NUMBER: US 08/905,144 FILING DATE: 1997-08-01 APPLICATION NUMBER: US 08/905,279
                                                                                                                                                                                          APPLICATION NUMBER: US 08/905,051 FILING DATE: 1997-08-01
                                                                                               APPLICATION NUMBER: US 08/904,468
                                                                                                                     FILING DATE: 1997-08-01
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Pred. No. 1.1e+02;
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SOFTWARE: Patent.pm SEQ ID NO 3325 LENGTH: 52

ORGANISM: Homo Sapiens

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; OTHER INFORMATION: US-10-631-441-3325
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                                                                           SOFTWARE: Patent.pm
SEQ ID NO 3330
LENGTH: 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -10-631-402-3330
Sequence 3330, Application US/10631402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/631,402
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US/09/547,599C
PRIOR FILING DATE: 2000-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
                                                                                                                                  PRIOR APPLICATION NUMBER: US 08/905,133 PRIOR FILING DATE: 1997-08-01 NUMBER OF SEQ ID NOS: 3475
                                                                                                                                                                                                PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,279
PRIOR APPLICATION PRIOR 08-01
PRIOR APPLICATION NUMBER: US 08/904,468
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR FILING DATE: 1997-08-01
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PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,135
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR APPLICATION NUMBER: US 08/905,144
PRIOR APPLICATION NUMBER: US 08/905,144
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OTHER INFORMATION:
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TILE OF INVENTION: Expressed Sequence Tags and
TILE REFERENCE: GEN-T119C1
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                        TYPE: PRT
ORGANISM: Homo Sapiens
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FEATURE:
OTHER INFORMATION: Cerebellum
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nes 4; Conserv
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Pred. No.
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; LOCATION: -47...1
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: SCORE 7.60
; OTHER INFORMATION: SEG CLATLTLEHTSFS/FQ
US-10-631-402-3330
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SOFTWARE: Patent.pm
SEQ ID NO 3330
LENGTH: 58
TYPE: PRT
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PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,135
PRIOR TILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,144
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,279
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,279
PRIOR FILING DATE: 1997-08-01
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Best Local S
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/631,441
CURRENT FILING DATE: 2003-07-30
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PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR FILING DATE: 1997-08-01
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                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Cerebellum
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  45 SFSF 48
                    1 SFSF 4
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milarity 100.0%;
Conservative 0
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Pred. No. 1.2e+02;
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                                                                                    Mismatches
                                                                                                       1.2e+02
                                                                                                                         DB 6;
                                                                                                                     Length 58
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RESULT 8
US-10-603-113-24077
; Sequence 24077, Application US/10603113
; GENERAL INFORMATION:

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US-10-603-113-24772
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US-10-603-113~23238
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                                                                                                             CURRENT APPLICATION UNMEER: US/10/603,113
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION UNMEER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 24772
LENGTH: 61
TWOSE-TO-
                                                                                                                                                                                                                                                                                                                           Sequence 24772, Appl GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
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LENGTH: 60
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                                                                                                                                                                                                                                          APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANTITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.132
                                                                TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
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PRIOR FILING DATE: 1999-02-12
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CURRENT FILING DATE: 2003-06-24
OTHER INFORMATION: Identity of amino acid sequences at the above locations
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PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ_ID NOS: 28206
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CURRENT FILING DATE: 2003-06-24
                     NAME/KEY: UNSURE
LOCATION: (7)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
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                                                                                    SEQ ID NO 150
LENGTH: 62
TYPE: PRT
ORGANISM: HO
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 Query Match
Best Local Similarity
Matches 4; Conserv
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LENGTH: 61
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Best Local
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APPLICANT: Keith Weinstock et al
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CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/10484
PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                        SOFTWARE: Custom
                                                                                                                                                                          NUMBER OF SEQ ID
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/808,701
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/668,680 PRIOR FILING DATE: 2000-09-22
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/540,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/603,113
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/695,618
                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND FILE REFERENCE: 790CIP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Nuvelo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 28206
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                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/728,711
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100.0%; Score 20; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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Pred. No.
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Pred. No. 1.2e+02;
; Mismatches 0;
 Mismatches
                1.3e+02;
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                                   DB 6;
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                                Length 62;
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SOFTWARE: Custom
SEQ ID NO 151
LENGTH: 62
TYPE: PRT
ORGANISM: Homo sapiens
US-10-291-128-151
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US-10-603-113-21539, Application US/10603113
SEQUENCE INFORMATION:
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
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Best Local S
Matches 4
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CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEO ID NOS: 28206
SEO ID NO 21539
LENGTH: 62
TYPE: PRT
                                                                                            Query Match
Best Local Similarity
                                                                            Matches
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PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/695,618
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 09/728,711
PRIOR FILING DATE: 2000-11-30
DETICA REDITATION N
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CURRENT APPLICATION NUMBER: US/10/291,128
CURRENT FILING DATE: 2002-11-08
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PRIOR APPLICATION NUMBER: PCT/US01/10484
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 172
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MERAL INFORMATION:
MERAL INFORMATION:
MITTLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
  58 SFSF 61
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                                      1 SFSF 4
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ilarity 100.0%;
Conservative 0.
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100.0%; Pred. No.
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Pred. No. 1.3e+02;
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Search completed: August 20, 2003, 12:45:13 Job time: 1.15663 secs
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US-10-603-113-23627
                                                                                                                                                 Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                SEQ ID NO 23627
LENGTH: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23627,
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/603,113
                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                          13 SFSF 16
                                                                                                             1 SFSF 4
                                                                                                                                                 Similarity 100.
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             2003-06-2
                                                                                                                                                                    100.0%;
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Pred. No. 1.3e+02;
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OM protein - protein search, using sw model Run on: August 20, 2003, 12:25:56; Search time 2.79518 Seconds (without alignments)
137.621 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Title: Perfect score: Sequence: US-09-512-082-30 20 1 SFSF 4

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

2222 2875 5	19 20 22 23 24	14 15 16 17	112 10 8	<b>765432</b> 1	Result
22222	222222	22222	222222	2222222	Score
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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
97	96	94	93	93	91	91	89	89	87	87	83	83	80	79	78
2	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
C75415	T29674	AE3247	AH1609	AD1247	T06963	в96574	JQ1822	C42525	D85803	G90954	T17809	C47188	S26991	T42000	D82182
nypothetical proce	•		_	_			5	A-ORF-P protein -	hypothetical prote		hypothetical prote	MHC class II histo	hypothetical prote	hypothetical proce	hypothetical prote

# ALIGNMENTS

SULT 3 3367 ctin - Macrotylom	Qy ' 1 SFSF 4 	Query Match 100.0%; Score 20; DB 2; Length 24; Best Local Similarity 100.0%; Pred. No. 78; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Ringuyen, C.K.; Gulliaume, C.E.; Nobers, C. Blochim. Biophys. Acta 1033, 210-213, 1990 A; Fittle: A blood group A specific lectin from the seeds of Crotalaria Striata. A; Reference number: S08292; MUID:90167102; PMID:2306467 A; Accession: S08292 A; Molecule type: protein A; Residues: 1-24 <ngu> A; Note: the source is designated as Crotalaria Striata C; Reywords: lectin</ngu>	RESULT 2 \$08292  lectin - smooth rattlebox (fragment) C:Species: Crotalaria pallida (smooth rattlebox) C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993 C:Accession: \$08292	Query Match 100.0%; Score 20; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 32; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 SFSF 4  Lili Db 5 SFSF 8	H.; Takahashi, 1993 Lion of novel 1 Lion entre 183993	RESULT 1 \$38305 Sectin GNL2 alpha chain - kidney bean (fragment) 1ectin GNL2 alpha chain - kidney bean) C;Species: Phaseolus vulgaris (kidney bean) C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997

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C;Genetics:
A;Gene: BH3
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C; Superf
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1993
C;Accession: A03367
R;Haylett, T.; Swart, L.S.
S. Afr. J. Chem. 35, 33-36, 1982
A;Reference number: A03367
A;Accession: A03367
A;Accession: A03367
A;Accession: A03367
A;Molecule type: protein
A;Residues: 1-32 <HAY>
C;Comment: This lectin from legume seeds is a tetramer of noncovalently bound identical e carbohydrates galactose, glucosamine, mannose, and fucose. It agglutinates erythrocyte c;Comment: This fragment is related to the amino end of the lentil lectin beta chain.
C;Comment: Dolichos axillaris (Macrotyloma axillare) is an African legume, also now grow c;Superfamily: plant lectin
                                                                                                                                                                                                                                                                                                                hypothetical protein BH3069 [imported] C:Species: Bacillus halodurans C:Date: 01-Dec-2000 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                          RESULT
E84033
                                                                                                         A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06788.1; A;Experimental source: strain C-125
                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-42 <STO>
                                                                                                                                                                                                          A; Reference number: A83650; A; Accession: E84033
                                                                                                                                                                                                                                                                                C; Accession: E84033
R; Takami, H.; Nakas
                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                              A; Title: Complete genome
                                                                                                                                                                                                                                                             R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Q
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A;Title: Structural requirements for the binding
A;Reference number: A48431; MUID:92361170; PMID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    닭
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agglutinin, EVA (N-terminal) - Erythrir C;Species: Erythrina variegata C;Date: 04-Sep-1998 #sequence_revision C;Accession: A48431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
A48431
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Best Local
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     100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                       sequence of the alkaliphilic bacterium 50; MUID:20512582; PMID:11058132
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 Score 20; DB Pred. No. 1.4
); Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                Bacillus halodurans (strain C-125)
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   1.4e+02; thes 0;
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                                     DB 2;
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                                                                                                                                                                                                                                      Bacillus halodurans
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                                                                                                       RESULT 8
G97539
                          hypothetical protein AGR_C_2731 [imported] - Agrobacterium tumefaciens (str. C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: G97539
             R; Goodner, B.;
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C; Keywords:
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A; Molecule type: DNA
A; Residues: 1-50 <HEI>
A; Cross-references: GB: AE004402;
A; Cross-references: GB: AE007402;
                                                                                                                                                                                                                                                          R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997 A;Tille: Complete nucleotide sequence of the chloroplast gen A;Reference number: Z15985; MUID:97303241; PMID:9159184
                                                                                                                                                                                                                                                                                                                         hypothetical protein 50 - Chlorella vulgaris chloroplast C;Species: chloroplast Chlorella vulgaris C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text. C;Accession: T07306
                                                                                                                                                               C; Genetics:
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A; Residues: 1-50 <WAK>
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Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein VCA0733 [imported] - Vibrio cholerae (strain N16961 serogroup C;Spectes: Vibrio cholerae C;Spectes: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: H82423
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H82423
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                                                           Score 20; DF Pred. No. 1.7); Mismatches
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Pred. No. 1.7
); Mismatches
                                                                                                                                                                           NID: g2224352; PIDN: BAA57954.1;
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                                                      DB 2;
. 1.7e+02;
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1.7e+02;
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H.; Dragoi,
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; Hinkle, Wollam, (

G.;

; Gattung, Allinger,

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Miller, N.; Blanchard, M.; Qurollo, Doughty, D.; Scott, C.; Lappas, C.;

B.; Gold Markelz,

Goldm

(strain C58,

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early protein gp6 - phage PZA

C:Species: phage PZA

A:Note: host Bacillus subtilis
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 23-Jul-1999
C:Accession: B29004
R:Paces, V.; Vlcek, C.; Urbanek, P.; Hostomsky, Z.
Gene 44, 115-120, 1986
A:Title: Nucleotide sequence of the right early region of Bacillus subtilis phage PZA.cc
A:Reference number: A91551; MUID:87031575; PMID:3095189
A:Accession: B29004
A:Molecule type: DNA
A:Residues: 1-54 <PAC>
A:Cross-references: GB:M11813; GB:M13904; GB:M13905; NID:g216046; PIDN:AAA88495.1; PID:g
C:Genetics:
A:Gene: 16.6
C:Superfamily: phage PZA early protein gp6
C:Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein NMB0517 [imported] - Neisseria meningitidis (strain MC58 serogroup C:Species: Neisseria meningitidis C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C:Accession: G81188
C:Accession: G81188
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fielschmann, R.D.; Dougherty, B.A.; Pi. Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V. A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Ccossion: G81188
A;Residues: 1-51 <TET>
A;Cross-references: GB:AE002408; GB:AE002098; NID:g7225740; PIDN:AAF40949.1; PID:g72257
A;Cross-references: GB:AE002408; GB:AE002098; NID:g7225740; PIDN:AAF40949.1; PID:g72257
A;Cenetics:
A;Gene: NMB0517
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A;Title: Genome Sequence of the Pl.
A;Reference number: A97359; MUID:2:
A;Accession: G97539
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <KUR>
A;Cross-references: GB:AE007869; P:
C;Genetics:
A;Gene: AGR_C_2731
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merty, B.
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A;Title: Nucleotide sequence of the right earl A;Reference number: J80192; MUID:89232766; PMI A;Accession: J50196
A;Molecule type: DNA
A;Residues: 1-54 <BEN>
A;Cross-references: GB:M28830; NID:g215438; PI C;Genetics:
A;Gene; 16.6
C;Superfamily: phage PZA early protein gp6
C;Keywords: early protein
hypothetical immunity region protein 11 (Species: Bacillus phage phi-105 A; Note; host Bacillus subtilis C;Date: 20-Aug-1999 #sequence_revision C;Accession: A27234 R;Cully, D.F.; Garro, A.J. Gene 38, 153-164, 1985
                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                             R;Garvey, K.J.; Yoshikawa, H.; Ito, J. Gene 40, 301-309, 1985
A;Title: The complete sequence of the Bacillus phage phi-29
A;Reference number: JN0030; MUID:86165872; PMID:3007295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             early protein gp6 - phage N; Alternate names: ORF 16. C; Species: phage phi-29 A; Note: host Bacillus amyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Benes, V.; Arnold, L.; Smrt, J.; Paces, V. Gene 75, 341-347, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: phage phi-15
A;Note: host Bacillus subtilis
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990
C;Accession: JS0196
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WRBPF6
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
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A; Residues: 1-54 <GAR>
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0; Mismatches 0;
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Pred. No. 1.8
); Mismatches
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); Mismatches
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                                                   20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                   A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84839
                                                                                                                                                                                                                                                                                                                                                                                                  R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, Leuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein At2g41230 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Dete: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84839
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Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlq
A;Reference number: Z15985; MUID:97303241; PMID:9159184
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A; Residues: 1-61 <STO>
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C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May_1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BAA57976.1; PID:g2224492
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A;Residues: 1-60 <WAK>
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100.0%; P7
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Pred. No. 1.9e+02;
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Search completed: August 20, 2003, 12:42:20 Job time : 4.79518 secs

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Minimum
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Maximum Match 100%
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    Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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length: 2000000000
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                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A.
-!- FUNCTION: May help in the
subunits (By similarity).
                                                                                                                                                                                                                                                                                                               MEDLINE=99398694; PubMed=10468594;
Turmel M., Otis C., Lemieux C.;
"The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: insights into the architecture of ancestral chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003
28-FEB-2003
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InterPro;
                 HAMAP; MF_00522;
                                     EMBL; AF137379; AAD54818.1;
                                                                                                                                                                                                                       -1- SIMILARITY: Belongs to the psaJ family
                                                                                                                                                                                                                                                                                                       genomes.";
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Chlorodendrales; Chlorodendraceae; Nephroselmis.
NCBI_TaxID=31312;
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InterPro; IPR001220; Lectin_legB.
Pfam; PF00139; lectin_legB; 1.
PROSITE; PS00307; LECTIN_LEGUME_BETA; IPROSITE; PS00308; LECTIN_LEGUME_ALPHA;
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HSSP; P05045; 1LU1.
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S. Afr. J. Chem. 35:33-36(1982).
-i- FUNCTION: METALLOGLYCODROTTEIN, CONTAINING CA, MG, J. THE CARBOHYDRATES GALACTOSE, GLUCOSAMINE, MANNOSE, AGGLUTINATES ERYTHROCYTES OF BLOOD GROUP Al.
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VG66_BPPH5
ID VG66_B
AC P15854
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DT 01-APR
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Early
GN 16.6.
OS Bacter
OC Viruse
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OX NCBI_T
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Viruses; dsDNA viruses,
phi-29-like viruses.
NCBI_TaxID-10755;
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MEDLINE-86165872; PubMed=3007295;

Garvey K.J., Yoshikawa H., Ito J.
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Viruses; dsDNA viruses,
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BEDLINE-89232766;
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Viruses; dsDNA viruses,
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"Nucleotide sequence of the immunity region o
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P10434;
MEDLINE=91338699; PubMed=2102378; Albani D., Robert L.S., Donaldson P.A., Altosaar Fabijanski S.F.; "Characterization of a pollen-specific gene famil napus which is activated during early microspore Plant Mol. Biol. 15:605-622(1990).
                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; books eurosids II; Brassicales; Brassicaceae.
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32, Last sequence up
32, Last annotation
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Pred. No.
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                                                                                                    family from Brassica
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YVAP_VI
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P20525;
01-FEB-1991
                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                 Hypothetical protein. sequence 89 AA; 9909
                                                                                                                                                                                    EMBL; M35027; AAA48170.1; PIR; C42525; C42525.
                                                                                                                                                                                                                                                                                                                                                                                           Goebel S.J.,
Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stag
Orthopóxvírus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ul-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical 9.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                          "Appendix to 'The complete DNA Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete DNA sequence of vaccinia virus."; Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goebel S.J., Johnson Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=91021027; PubMed=2219722;
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PIR; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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63 AA;
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Johnson G.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                     Perkus M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA stage;
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                                                                                    Score 20; DE
Pred. No. 1.4
0; Mismatches
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                                                                                                                                                 399EA9270DF3E75A CRC64;
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Pred. No.
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                                                                                                                   Length 89;
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                                                                                                                                                                                                                                                                                          restrictions
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RESULT 11
POL_HV1J3
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YCXF_CYAPA
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Best Local S
Matches 4
                                                                                                                                                                                   POL_HV1J3
P12498;
01-OCT-1989
01-OCT-1996
28-FEB-2003
 MEDLINE-89352108; Pul
Komiyama N., Hattori
                                  SEQUENCE FROM
                                                                Human immunodeficiency Viruses; Retroid viruse Viruses; Retroid viruse VICBI_TaxID=11694;
                                                                                                                                                  POL polyprotein [Conta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
PIR; ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-UTEX LB 555 / Pringsheim;
Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella
Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
"The complete sequence of the cyanelle genome of Cyanophora p
the genetic complexity of a primitive plastid.";
(In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
Schwemmler W. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996
01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Cyanelle. SEQUENCE 91 AA; 11166 MW; 6
                                                                                                                                    (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotism and Symbiosis, pp.40-48,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bryant D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=UTEX LB 555 / Pringsr
Stirewalt V.L., Michalowski
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P48336;
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NCBI_TaxID=2762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical 11.2
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                                                                                                                                                (Rel. 12, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
tein [Contains: Protease (Retropepsin)
nscriptase (EC 2.7.7.49); Ribonuclease
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                                                                                                                                                                                                                                                       STANDARD;
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                                                                                     viruses;
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PubMed=2669897;
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alowski C.B.,
                                                                                   virus type 1 (JH
es; Retroviridae;
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Last sequence update)
Last annotation updat
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
Sakuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Loeffelhardt W., Bohnert H.J.,
                                                                                   (JH3 isolate) (HIV-1)
dae; Lentivirus.
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Kurimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
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Τ.,
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                                                                                                                                                  .4.23.16);
3.1.26.4)]
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Yoshida M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collaboration
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SO TITES AND DESCRIPTION OF THE SERVICE OF THE SERV
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  RESULT 12
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /_METJA
Y067_METJA
Q60371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00141; ASP_PROTEASE; 1.

PROSITE; PS00141; ASP_PROT_RETROV; 1.

ALDS; Polyprotein; Hydrolase; Aspartyl protease; En Nuclease; Transferase; RNA-directed DNA polymerase. CHAIN 57 >100

ACT_SITE 81 81 81 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequences of gag and env genes of a Japanese isolate HIV-1 and their expression in bacteria."; AIDS Res. Hum. Retroviruses 5:411-419(1989).
-1- CATALYTIC ACTIVITY: Specific for a PI residue that is hydrople.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and P1' variable, but often Pro. - CATALYTIC ACTIVITY: Endonucleolytic cleavage
                      MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                         Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Met
Methanocaldococcaceae; Methanocaldococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001995; Aspprotease_rtrv.
InterPro; IPR001969; Aspprotease_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV; M21137; POL$JH3.
MEROPS; A02.001; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical MJ0067.
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2190;
"Complete genome jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DETERMINED.
SIMILARITY: THE PROTEASE BELONGS
KNOWN AS THE RETROPERSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphomonoester.

CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N
+ (DNA)(N).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53
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4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                                                                                   43067;
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Best Local S
Matches 4
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01-NOV-1997
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus

Jannaschii.";

Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 273:1058-1073(1996).
-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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TRANSMEM 6 21
TRANSMEM 34 5.
TRANSMEM 79 9.
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                                                                         EMBL; U67469; PIR; C64315;
                                        TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2190;
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PF04930; FUN14; 1.
Pro+ical protein; Transmembrane;
                                        MJ0123;
                                                                                                                  U67469; AAB98111.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein MJ0123.
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; 94DCD5C2F9394D53 CRC64;
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Pred. No. 1.6
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protein;

Complete

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SEQUENCE

110

AA:

13187 MW;

B905F6BBFBF207DF CRC64;

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RESULT 15
Y465_AQUAE
ID Y465_A
AC 06676
AC 16-0C
DT 16-0C
DT 16-0C
DT 16-0C
DE Hypot
GN AQ_46
OS AQUIF
GN AQ_46
OS AQUIF
GN RESULT
RN [1]
RR SEQUE
RC STRAI
RA Decke
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YGC4_Y YEAST
ID YGC4_Y AC P53190
DT 01-OCT
CC Saccha
OX Saccha
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RN [1]
RP SEQUEN
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RL Submit
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                                                                                                                                                                                                                                                            066767;
16-OCT-2001
16-OCT-2001
16-OCT-2001
MEDLINE=98196666; PubMed=9537320; Deckert G., Warren P.V., Gaasterl
                                                                                                                                                                                                                                                                                                                                                        AQUAE
Y465_AQUAE
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SEQUENCE
                                                                                                                                   Bacteria; Aquificae; NCBI_TaxID=63363;
                                                             STRAIN-VF5
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P53190;
O1-OCT-1996 (Rel. 34, Created)
O1-OCT-1996 (Rel. 34, Last sequence update)
O1-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 12.2 kDa protein in PGD1-STT3 intergenic region.
YGL024W.
                                                                                                                                                                                    Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein;
TRANSMEM 22 4;
TRANSMEM 48 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hebling U., Hofmann B.,
Submitted (MAY-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 272547; CAA96726.1;
S64026; S64026.
S0002992; YGL024W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 AA;
                                                                                                                                                                                                                        (Rel. 40, Created)
(Rel. 40, Last sequence.update)
(Rel. 40, Last annotation update)
protein AQ_465.
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75
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68 P
95 P
12210 MW;
                                                                                                                                                     Aquificales; Aquificaceae; Aquifex
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the EMBL/GenBank/DDBJ databases.
       Gaasterland
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Pred. No. 1.7e+02;
Mismatches 0;
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Pred. No. 1.7e+02;
Mismatches 0;
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       Young W.G.,
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     Lenox A.L.,
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                                                                                                                                                                                                                                                                                                                                                                       Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                            Hypothetical protein;
TRANSMEM 7 29
                                                                                                                                                                            EMBL; AE000691; AAC06729.1; -. PIR; C70342; C70342.
                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        Nature 392:353-358(1998).
73 SFSF 76
                              1 SFSF 4
                                                              Similarity 4; Conserv
                                                                                                                           113 AA;
                                                              Conservative
                                                                                                                            13252 MW;
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Pred. No.
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Search completed: August 20, 2003, 12:34:56 Job time: 4.62918 secs

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Maximum Match 100%
Listing first 45 summaries
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protein search, using sw
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length: 2000000000
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136.423 Million cell updates/sec
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Gapop 10.0 ,
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sp_bacter1a:*
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sp_rvirus:*
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Q8EZR7
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Q9FB83
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Q49491 mycoplasma
Q9k8d7 bacillus ha
Q8ezr7 leptospira
Q8sm41 spatoglossu
Q60031 aspergillus
Q8kb18 chlorobium
Q9fb83 helicobacte
Q9fb93 helicobacte
Q9k110 vibrio chol
                                                                             Q988)5 psophocarpu
Q988)2 phaseolus v
Q96912 homo sapten
Q45547 bacillus su
Q8666 homo sapten
Q986x8 erythrina v
Q91fb5 chilo iride
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	Q86747 leptospira Q86747 leptospira Q8aev7 human immun Q9pbb3 xylella fas Q8aev9 human immun Q8aev9 human immun Q8aev5 human immun	lumpy skin entamoeba h drosophila dictyosteli arabidopsi arabidopsi blasmodium plasmodium	Q8u5a9 agrobacteri Q05977 synechocyst Q9k0r3 neisseria m Q57376 leptospira Q8f2z7 leptospira Q9x559 enterococcu p92500 apis mellif p92499 apis mellif p92491 apis mellif Q8hq03 thrips imag Q8g202 arabidopsis

### ALIGNMENTS

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Q9SBJT 1
Q9SB AC Q9SB
AC Q9SB
DT 01-M

Query Match
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Matches 4
Q9S8B2
Q9S8B2;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2002
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Q9S8J5; Q1-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheor
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tetragonolobus (L.) DC.";
Plant Cell Physiol. 35:1087-1095(1994).
SEQUENCE 20 AA; 2363 MW; 1BF1B347020D3DCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-95120285; PubMed-7820375;
Yagi F., Sawada R., Imada T., Toyonaga S., '
"Two isolectins from leaves of winged bean,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Psophocarpus.
NCBI_TaxID=3891;
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                                                                                                                                                                                                                                                                                                          5 SFSF 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
(TremBLrel. 13, Created)
(TremBLrel. 13, Last sequence update)
(TremBLrel. 21, Last annotation update)
                                                                                                                                        PRELIMINARY;
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2.3e+02;
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RESULT Q45547
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Q45547;
01-NOV-1996
STRAIN-W23;
Harry E.J., Partridge S.R.,
"divIB region of Bacillus li
Submitted (NOV-1993) to the
EMBL; L25649; AAA72410.1; -.
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01-OCT-2002
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Q96G12;
01-DEC-2001
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Bacteria; Firmicutes;
NCBI_TaxID=1423;
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01-DEC-2001
                                                                                                                                                 SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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NON_TER 1
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Homo sapiens (Human).
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Kamemura K., Furuichi Y., Umekawa H.,
"Purification and characterization of
bean, Phaseolus vulgaris L.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNL-2 alpha subunit (Fragment).

Phaseolus vulgaris (Ridney bean) (French bean).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
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(TrEMBLrel. 22,
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2476 MW;
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2399 MW; B09E883F93CCD833 CRC64;
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Pfam; PF00139; lectin_legB; 1.
ProDom; PD000711; Lectin_legB; 1.
                                                                                                                                                            Erythrina variegata (Coral tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoldeae; Phaseoleae; Erythrina.
NCBI_TaxID-3845;
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01-MAY-2000 (TremBLrel.
01-MAR-2002 (TremBLrel.
                                                                        "Structural requirements for the binding of oligosaccharides immobilized lectin of Erythrina variegata (Linn) var. orienta Slycoconj. J. 7:311-322(1990).
ISSP: P16404; 1AX2.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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SEQUENCE
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Submitted (MAY-2002)
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Schnitzler P., Soltau J.B.
Delius H., Darai G.;
Molecular cloning and phy
iridescent virus type 6: fi
the viral genome.";
Virology 160:66-74(1987).
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Q91FB5;
Q1-DEC-2001
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MEDLINE-86174607; PubMed-
Lorbacher de Ruiz H., Gel
"Insect iridescent virus
in mice.":
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"DNA analysis of insect iridescent virus
permutation and terminal redundancy.";
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 Schnitzler P., Hug M.,
Delius H., Darai C.;
"Identification of gene
                              SEQUENCE FROM N.A.
MEDLINE-94167241; PubMed-8121799;
                                                              Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.; "Identification of the gene encoding the major capsid protein insect iridescent virus type 6 by polymerase chain reaction."; J. Gen. Virol. 74:873-879(1993).
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"The DNA sequence of Chilo iridescent virus between coordinates 0.101 and 0.391; similarities in coding insect and vertebrate iridoviruses.";
Virus Genes 15:235-245(1997).
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MEDLINE-94292906; Sonntag K.C., Muller
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"Insect iridescent virus type 6 encodes a polypeptide largest subunit of eukaryotic RNA polymerase II.";
J. Gen. Virol. 75:1557-1567(1994).
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                                                Jakob N.J., Mueller K., Bahr
Jakob N.J., Mueller K., Bahr
Submitted (SEP-2000) to the
EMBL; AF303741; AAK82269.1;
SEQUENCE 41 AA; 4991 MW;
                                                                                                                          MEDLINE-21342589; PubMed-11448171;
Jakob N.J., Muller K., Bahr U., Darai G.;
"Analysis of the First Complete DNA Sequence
Iridovirus: Coding Strategy of the Genome of
Virology 286:182-196(2001).
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"Identification of a thymidylate synthase
Chilo iridescent virus.";
Virus Genes 17:243-258(1998).
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Bahr. U., Tidona C
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virus Genes 18:243-264(1999).
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MEDLINE-99125223;
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EMBL; AP001517; BAB06788.1:
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STRAIN-C-125 / JCM 9153;

MEDLINE-20512582; PubMed-11058132;

Takami H., Nakasone K., Takaki Y., Maeno G.

Tuji F., Hirama C., Nakamura Y., Ogasawara
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Peterson S.N., Schramm N., Hu P.C., Bott K.F.,
"A random sequencing approach for placing mark
of Mycoplasma genitalium.";
Nucleic Acids Res. 19:6027-0031(1991).
EMBL; X61539; CAA43751.1; -.
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Random genomic sequence MC14 (Fragment).
Mycoplasma genitalium.
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4.7e+02;
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01-AUG-1998 (
01-AUG-1998 (
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Hypothetical
Aspergillus n
                                                060031;
                                                                                                                                                                                                                                  "A phylogenetic relationship among the genera of Dictyotaceae (Dictyotales, Phaeophyta) based on partial rbcL sequences."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF353382; AAMO8198.1; -InterPro; IPR002160; Kunitz_legume. InterPro; IPR000894; RuBisCO_small. Pfam; PF00101; RuBisCO_small; 1.
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01-JUN-2002 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
Ribulose-1,5-biphosphate
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Lee W.J., Bae K.S.;
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                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=157007;
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STRAIN=56601 / Serogroup
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1 5.7 kDa protein
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6 AA;
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RUBISCO_SMAIl; 1.
190; RUBISCO_SMAIL; 1.
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39 MW; B3374E64EBE8AlD6 CRC64;
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21, Last sequence update)
23, Last annotation update)
23 carboxylase small subunit (Fragment).
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XX MEDLINE-22103685; PubMed-121093901;
XX Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
XX Dodson R.J., Debby R., Gwinn M.L., Nelson W.C., Haft D.H.,
XX Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
XX Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
XX Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
XX Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
XY Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
XY The complete genome sequence of Chlorobium tepidum TLS, a
Yenter J.C., anaerobic, green-sulfur bacterium.";
XX Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
XX R. TIGR; CT1980; T.
                                                                                                                                          Query Match
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Q8KB18;
Q1-OCT-2002 (TrEMBLrel. 22, Cr
Q1-OCT-2002 (TrEMBLrel. 22, La
Q1-OCT-2002 (TrEMBLrel. 22, La
Q1-OCT-2002 (TrEMBLrel. 22, La
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MEDLINE-20309321; PubMed-10852481;

Van den Bink J.M., Punt P.J., Van Gorcom R.F.M.,

Van den Hondel C.A.M.;

Van den Hondel C.A.M.;

**Regulation of expression of the Aspergillus niger benzoate |
hydroxylase cytochrome P450 system.";
hydroxylase cytochrome P450 system.";
Mol. Gen. Genet. 263:601-609(2000).

**EMBL; AJ005117; CAA06381.1; -.
Hypothetical protein.

**SEQUENCE 48 AA; 5746 MW; EB85F2B8CA0B1CDD CRC64;
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                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                        Hypothetical protein; Complete proteome.
SEQUENCE 48 AA; 5801 MW; 4A3D5E7EE14A77DD CRC64;
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van Zeijl C., Brons
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Pred. No. 5.4e+02;
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'A M(r) 34,000 proinfilammatory outer membrane pr
Helicobacter pylori.";

Proc. Natl. Acad. Sci. U.S.A. 97:7533-7538(2000)
EMBL; AF233670; AAG00390.1; -.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
                                                                                                                         SEQUENCE
                                                                                                                                           Helicobacter pylori.";
Proc. Natl. Acad. Sci. U.S.A.
EMBL; AF233660; AAG00380.1; -
                                                                                                                                                                                                                                              Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori (Campylobacter pylori).
                                                                                                                                                                         Yamaoka Y., Kwon D.H., Graham D.Y.; "A M(r) 34,000 proinflammatory outer membrane protein (oipA) of
                                                                                                                                                                                              MEDLINE-20319061;
                                                                                                                                                                                                          STRAIN-JK23
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D.H., Graham D.Y.;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen

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Minimum DB
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              UlA protein derive
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H. pylori 26 kDa p
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liver age	020001144	၁ ၁	Z,	100 0	) )	ה ה
digestiv	AAM92954	22	68	100.0	26	44
Human ORFX protein	ABP08962	23	66	100.0	26	3
•	ABP39857	23	66	100.0		
Human secretory po	ABP75387	24	62	100.0	26	41
Human GENSET prote	ABP76248	24	60	100.0	26	0
Human novel foetal	AAU20693	22	59	100.0	26	39
breast	AAY48523	20	56	100.0	26	38
Human novel secret	ABG95299	23	53	100.0	26	37
Human secreted pro	AAW74848	19	53	100.0	26	36
Arabidopsis thalia	AAG55535	21	52	100.0	26	35
Human ORF4431 prot	ABP35458	23	51	100.0	26	34
Human kidney relat	AAM42609	22	51	100.0	26	33
excretory r	AAM99794	22	51	100.0	26	32
-	ABB14820	22	51	100.0	26	3
Human polypeptide	AAO10716	22	50	100.0	26	30
secreted	AAB24535	21	48	100.0	26	29
Human secreted pro	AAY91367	21	47	100.0	26	28
Peptide #12385 enc	AAM38348	22	39	100.0	26	27
	AAM65444	22	39	100.0	26	26
Human liver peptid	ABG59752	22	39	100.0	26	25
A TSAR-13 peptide	AAR58363	15	39	100.0	26	24
an hist	AAW31678	19	38	100.0	26	23
fungal and	AAW19444	18	38	100.0	26	22
-fungal	AAW19427	18	38	100.0	26	21
Full length human	AAR89894	17	38	100.0	26	õ
Group B Streptococ	AAU03617	22	36	100.0	26	[9
idopsis	AAG59652	21	36	100.0	26	<u></u>
eptococci	ABP30850	23	32	100.0	26	17
export sig	AAR59870	15	28	100.0	26	9
fungal and	AAW19428	18	27	100.0	26	5
and	AAW19473	18	27	100.0	26	4
INTERC	AAB66072	22	23	100.0	26	ա
50	AAG77700	22	22	100.0	26	5
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#### ALIGNMENTS

RESULT 1 AAB10067 UlA protein derived tryptic peptide #6 AAB10067 standard; peptide; 9 Unidentified. UlA protein; 03-NOV-2000 AAB10067; WPI; 2000-400193/34. WO200031544-A1 (XERI-) XERION PHARM GMBH. 24-NOV-1998; 23-NOV-1999; 02-JUN-2000 LL, Ng (first entry) tryptic peptide; functional site; 98DE-1054196 99WO-EP09052 B detection

Identifying functional sites in proteins, useful for detecting epitopes and ligand binding sites, by complexing with tagged binding partner, then laser irradiation to alter the protein close to the tag

Example

24;

41pp; German

invention describes a novel method for identifying one or

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RESULT 2
AAB10068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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functional sites in a target protein (I) which comprises: (i) complexing (I) with a binding partner (A) that carries a laser-activatable tag; (ii) irradiating the complex (II) formed with laser light to generate free radicals that alter bound (I) selectively at the binding sites; and (iii) identifying the altered region by a combination of protein cleavage and mass spectrometry (MS). The method is used to identify any type of
                                                                                                                                                                            Identifying functional sites in proteins, useful for detecting epitopes and ligand binding sites, by complexing with tagged binding partner, then laser irradiation to alter the protein close to the tag
                                                                                                                                                                                                                                                                                       Ilag
                                                                                                                                                  Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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                                                                                                                                                2; Page 24; 41pp;
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                                                                                                                                                 This invention describes a novel method for identifying one or more functional sites in a target protein (I) which comprises: (i) complexing (I) with a binding partner (A) that carries a laser-activatable tag; (ii) irradiating the complex (II) formed with laser light to generate free radicals that alter bound (I) selectively at the binding sites; and (iii) identifying the altered greion by a combination of protein cleavage and mass spectrometry (MS). The method is used to identify any type of functional site in any type of protein but particularly ligand-binding sites and epitopes: It can also be used to investigate pathologically altered proteins. The method does not require knowledge of the three-dimensional structure of (I), and is simple, rapid and automatable. It can identify non-linear or discontinuous entropy and determined the content of the
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                                                                             It can identify non-linear or discontinuous epitopes, and deprotein function without inactivation of (I) (since the tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying functional sites in proteins, useful for detecting epitc and ligand binding sites, by complexing with tagged binding partner, then laser irradiation to alter the protein close to the tag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (XERI-) XERION PHARM GMBH.
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Query Match Best Local Matches .

Similarity

100.0%;

Score 26; DB Pred. No. 54; ); Mismatches

54; В 21; 0;

Length 13; Indels

0;

Gaps

0

4;

Conservative

0:

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RESULT 5
AABIJO003
ID AABIJO003
ID AABIJO003
ID AABIJO003
ID AAC AABIJOO003
ID AAC AABIJOOU03
ID AAC AABIJOOU
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                                                    chinection by an acid-resistant microorganism (A) by treating a faecal confection by an acid-resistant microorganism (A) by treating a faecal confection by an acid-resistant microorganism (A) by treating a faecal confection with at least two different monoclonal antibodies (MAb) (or their fragments or derivatives) or aptamers (collectively (I)) and detecting conference of the first and second (I) bind to epitopes of different antigens (C) (Ag). These epitopes are present, after passage through the intestines, conference or immunized with (A), or its extract, lysate, derived protein confered or immunized with (A), or its extract, lysate, derived protein conference or immunized with (A), or its extract, lysate, derived protein conference or fragment, or with a synthetic peptide. Practically all mammals display at least one of the specified epitopes. The method is used to detect confection by acid-fast bacteria, particularly of the genera Helicobacter, conference of the specified epitopes. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible conference represents a fragment of a H. pylori 26 kba protein-binding antibody heavy chain complementarity determining region CDR3 which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. pylori 26 kDa protein-binding antibody heavy chain CDR3 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         petecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a faecal sample with two binding reagents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAB10003
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06-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Page 21; 84pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigens that survive intestinal passage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reiter C,
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      Sequence
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          13 AA;
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98EP-0120687.
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RESULT 6
ARABIO071
ID AAB;
XX AAB;
XX AAB;
XX U1A
                                               RESULT 7
AAE02857
ID AAE0
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                                                                                                                                                                                                                                                                                                                                               This invention describes a novel method for identifying one or more C functional sites in a target protein (1) which comprises: (1) complexing C(1) with a binding partner (A) that carries a laser-activatable tag; (1i) cradiating the complex (II) formed with laser light to generate free CC radicals that alter bound (I) selectively at the binding sites; and (iii) C identifying the altered region by a combination of protein cleavage and CC mass spectrometry (MS). The method is used to identify any type of CC functional site in any type of protein but particularly ligand-binding CC sites and epicopes. It can also be used to investigate pathologically CC altered proteins or oncogenic proteins, and to inactivate target CC pathological proteins. The method does not require knowledge of the CC three-dimensional structure of (I) and is simple, rapid and automatable. CC tran identify non-linear or discontinuous epitopes, and determines CC protein function without inactivation of (I) (since the tag is bound to CC (A) not to (I) itself). The method may be used in vitro or in vivo for Studying intra- or extra-cellular proteins. This sequence represents a complete continuous discontinuous epitopes and determines complete the tag is bound to continuous discontinuous epitopes.
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Best Local (
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        AAE02857;
                                         AAE02857 standard; peptide;
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying functional sites in proteins, useful for detecting epitopes and ligand binding sites, by complexing with tagged binding partner, then laser irradiation to alter the protein close to the tag
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                                                                                                                                                                                                                                                                                                                                           of the invention
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                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                   FPFY 4
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                                                                                                                                                                                                                                                                                                        8
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                                                                                                                                                                                                                      Score 26; DE
Pred. No. 54;
); Mismatches
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                                                                                                                                                                                                                                          54;
                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                         Length 13;
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                                                                                                                                                                                                                    Gaps
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10-AUG-2001

(first entry)

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RESULT 8
AAE02910
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                          Matches
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17-DEC-1999;
27-JAN-2000;
03-MAY-2000;
10-NOV-2000;
AAE02910;
                                                      AAE02910 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel breast cancer-associated proteins and nucleic acids encoding proteins useful for diagnosing, treating breast cancer and as indicators for monitoring the efficacy of breast cancer therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 43; Page 41; 64pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MATR-) MATRITECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-AUG-2001 (first entry)
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                                                                                                                                                                                                                FPFY 8
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                                                                                                                                                                                                                                                                                                                                100.0%; ilarity 100.0%; Conservative 0
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; 2000US-0201721.
; 2000US-0172170.
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99US-0172170
                                                      peptide;
                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                Score 26; DB
Pred. No. 54;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             Length 13;
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Tryptic peptide #1

of.

human U2 small nuclear ribonucleoprotein

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RESULT 9
AAO26562
ID AAO2
XX
AC AAO2
AC AAO2
DT 06-M
XX
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                                                                                                                                                                                                                                                                                                                                     The present invention relates to marker molecules indicative of disease in mammals which are identified using a new method in which an abundant protein is removed from a sample to enable less abundant molecules to be evaluated as possible markers, the sample is then fractionated and fractions analysed by known mass spectroscopy techniques and results compared between individuals with and without the disease. The method is useful for identifying disease markers in mammals, especially humans, cespecially markers for cancer, such as breast, lung, prostate, bladder, cervical, ovarian, colon or colorectral cancer. Once identified, the markers can be used as targets in assays for detecting the disease and in disease treatment e.g. administration of antibodies binding to and cellminating/reducing activity of the target protein in vivo. The present sequence is a tryptic peptide of human U2 small nuclear ribonucleoprotein B (U2 snRNP B) which is used in the invention. The peptide is obtained from U2 snRNP B by proteolysis with trypsin.

Note: The present sequence is also shown in sequence listing of the specification, but lacks an amino acid in the N-ternimal end and in the
                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 4
               Threonine synthetase 13.75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spectroscopy based methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identification of disease markers in mammals, especially cancer markers useful as targets in methods for detecting or treating cancer, by removing an abundant protein from a sample and analyzing by mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watkins BA;
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U2 small nuclear ribonucleoprotein
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03-MAY-2000;
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17-DEC-1999;
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                                            06-MAR-2003
                                                                         AA026562;
                                                                                                   AAO26562 standard;
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example
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                                                                                                                                                                             σ
                                                                                                                                                                                                                                    4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Page 26; 46pp; English
                                                                                                                                                                           FPFY 4
                                                                                                                                                                                                                                                                                                                           end.
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; 2000US-0201721.
; 2000US-0172170.
                                                                                                                                                                                                                                       Conservative
                                            (first entry)
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99US-0172170
                                                                                                   Peptide; 15
                                                                                                                                                                                                                                                  100
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n; colorectal; tryptic peptide; proteolysis;
cleoprotein B; U2 snRNP B; trypsin.
                                                                                                                                                                                                                                                   .0%;
               protein
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                                                                                                                                                                                                                                                   Score 26;
Pred. No.
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                                                                                                                                                                                                                                    red. No. 62;
Mismatches
               N-terminal peptide region
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RESULT 10
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Best Local (
16-JUN-2000;
17-OCT-2000;
16-MAR-2001;
                                                                                                                               BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosypressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritts; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention also relates to the polynucleotide for coding it, the proceeding preparing the polypeptide by DNA recombination technique, the application of the polypeptide in treating several diseases such as cancer, HIV infection, the antagonist against this polypeptide and it therapeutic action, and the application of said polynucleotide to cothis new threonine synthetase 13.75. This sequence represents an N-terminal peptide region of the threonine synthetase 13.75 protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                     WO200202641-A1
                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                 19-AUG-2002
                                                                                                                                                                                                                                                       ABP46251;
                                                                                                                                                                                                                                                                            ABP46251 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptide-threonine synthetase 13.75 and polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-2000;
                                            15-JUN-2001;
                                                                  10-JAN-2002
                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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2000US-212210P.
2000US-240816P.
2001US-276248P.
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                            2001WO-US19110
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62;
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RESULT 11
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity much be associated with aberrant acceptance of BLyS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 repretible antibodies and fragments of the antibodies described in the met
                        Human discs large 1 gene family - useful in,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies against B Lymphocyte the diagnosis and treatment of c
  composition(s)
                                                                                                                                (SUME ) SUMITOMO ELECTRIC IND
                                                                                                                                                                                  23-AUG-1996;
                                                                                                                                                                                                                                  23-AUG-1996;
                                                                                                                                                                                                                                                                                     10-MAR-1998
                                                                                                                                                                                                                                                                                                                                        JP10066581-A
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          internal secretion tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; NE-dlg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NE-dlg SEQ ID
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25-MAY-2001; 2001US-293499P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a unour necrosis factor (TNF) super family and induces
                                                                             1998-224339/20.
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CAMBRIDGE ANTIBODY TI
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llarity 100.0%;
Conservative (
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for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide;
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     cancer
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Pred. No.
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                        therapeutic
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Best Local
                                              AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletion in a patient's genome that affect the activity of P by expressing
                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a NE-dlg molecule. The present invention describes human discs large I gene (dlg) family expressible in nerve tissue. Also described are: (1) a polynucleotide (PN) encoding dlg and comprising a 3100 (I) or 3213 bp (II) sequence; (2) RNA corresponding to PN having a sequences (I) and (II); (3) RNA having a base sequence translated by dlg; (4) an antisense PN having a at least 15 bp sequence, and which is a part of PN of (1); (5) a derivative of the antisense PN; (6) an antibody specific for dlg, and (7) an antibody specific for a polypeptide having a 817 or 849 an sequence. The polypeptide, RNA's and antibodies can be used for detection of dlg. The antisense PN can be antisense PN can be
inactive proteins or to supplement the patients own production Additionally, N may be used to produce the colon cancer-associa
                                                                                                                                                                                                                                                                                                                       Claim 11; Page 9724; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-SEP-1999;
03-NOV-1999;
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and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention.

N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                           The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see ARF45121-F45136 and ARF45138-F45139 and ARB66037, ARB66037, and ARB66083 and ARB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders system (CNS) disorders, CNS-related disorders include hearing signal and cerebrovascular disorders and other neurological and cerebrovascular disorders. The CNS disorders include nlzhelmer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders,
                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McCarthy SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-1999;
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                            neuropsychiatric disorders, psychoactive substance use anxiety, and bipolar affective disorder.
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CC D-amino acid histatin 2, found in human paratiol secretion, where at CC least one amino acid in the peptide is in the D-configuration. The CC peptide is preferably modified by an acetyl or carbamyl addition at the C-terminus and/or amidation at the C-terminus. The novel D-amino CC acid-containing peptide, based on the naturally occurring histidine-CC rich human histatins, have anti-fungal and anti-bacterial activity and CC are useful in compositions for the treatment of oral, vaginal, urethral, CC mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial cc infections. It is particularly effective against local and systemic CC candida albicans infection, against oral bacterial diseases such as CC caries and periodontitis (by inhibiting e.g. Streptococcus mutans and CC porphyromonas gingivalis) and against Clostridium histolyticum. The D-CC amino acid-containing peptide has superior anti-fungal (especially canti-candidal) and anti-bacterial activity, particularly on a weight basis, compared to the natural L-amino acid forms of histatins and CC histatin-based peptides. The presence of D-residues also makes the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida albicans, peridontitis; carles; to vaginal infection; urethral infection; murespiratory infection; skin infection; observed the control of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW19473;
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                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an anti-fungal and anti-bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   histatin-based peptide(s) - us infections, periodontitis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-fungal and anti-bacterial D-amino histatin-based peptide(s) - useful esp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-052234/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Friden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
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1..27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peridontitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roberts FD,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tooth decay; oral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spacciapoli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porphyromonas gingivalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 멂
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RESULT 15
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Best Local
The present sequence represents histatin 2, found in human paratoid secretion, where at least one amino acid is in the D-configuration. The peptide preferably is modified by an acetyl or carbamyl addition at the N-terminus and/or amidation at the C-terminus. The peptide, based on the naturally occurring histidine-rich human histatins, have anti-fungal and anti-bacterial activity and are useful in compositions for the treatment of oral, vaginal, urethral, mucosal respiratory, skin, ear and ophthalmic fungal or bacterial infections. It is particularly effective against local and systemic Candida albicans infection, against oral bacterial diseases such as caries and periodontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas gingivalis) and against Clostridium histolyticum. The peptide has
                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
01-NOV-1991;
28-OCT-1993;
09-AUG-1994;
                                                                                                                                                                                             Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for treating Candidal infections, periodontitis and caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       respiratory infection; skin infection; mucosal infection; ear infection; bacterial disease; Streptococcus mutans; Porphyromonas gingivalianted Clostridium histolyticum: human
                                                                                                                                                                        Disclosure; Fig 1; 72pp; English.
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                                                                                                                                                                                                                                                                             Friden PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-fungal and anti-bacterial histatin-based histatin 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-SEP-1997
                                                                                                                                                                                                                                                                                                       (PERI-) PERIODONTIX INC. (UYBO-) UNIV BOSTON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptides more resistant to degradation than corresponding L-amino acid versions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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91US-0786571.
93US-0145030.
94US-0287717.
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                                                                                                                                                                                                                                                                            Roberts FD,
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                            Spacciapoli P;
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Best Local
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                                                                                                                         superior anti-fungal (especially anti-Candidal) and anti-bacterial activity, particularly on a weight basin, compared to the longer, naturally occurring histatins. Peptides containing D-residues are also more resistant to degradation than L-amino acid versions.
                                                                                                   Sequence
13 FPFY 16
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Pred. No. 1.1
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1.1e+02;
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Search completed: August 20, 2003, 12:33:45
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Listing first 45 summaries
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Maximum DB
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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length:
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        US-08-441-914-14
US-08-485-273A-2
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US-08-98-717-9
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US-08-485-273A-1
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US-09-199-637A-9	US-08-449-731-6	US-08-450-582-6	US-08-865-336-4	US-08-452-655B-6	US-08-452-654-6	US-08-289-548A-6	US-07-741-940-6	US-08-865-336-1	US-09-149-476-565	US-09-732-210-675	US-09-083-352-10	US-09-083-352-8	US-09-083-352-6	US-09-083-352-5	US-09-083-352-4	US-09-083-351-10	US-09-083-351-8
Sequence 9, Appli	Sequence 6, Appli	•	Sequence 4, Appli	Sequence b, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 1, Appli	Sequence 565, App	•••	Sequence 10, Appr		Sequence 6, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 10, Appl	8, A

ALIGNMENTS

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; MOLECULE TYPE: peptide US-08-287-717-14
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                                                                                                                                                                                                 APPLICATION UNDER: US/08/287,717
APPLICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,030
APPLICATION NUMBER: US/08/145,030
APPLICATION NUMBER: US/07/786,571
APPLICATION INFORMATION:
NAME: Granahan, Patticia
NAME: Granahan, Patticia
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: BU91-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-5240
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                                                                                                                                                          TELEPHONE: 617-861-62/
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                         SEQUENCE CHARACTERISTICS:
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CITY: Lexington
STATE: Massachus
                                                                               amino acid
GY: linear
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                                                                                                                     6 amino acids
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Length 6;
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Score 26; DB 1; Pred. No. 2.5e+05; ; Mismatches 0;

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                                                                        Designation US/08481888A Patent No. 5631228
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Best Local :
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Sequence 14, App...
                    APPLICANT:
APPLICANT:
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      APPLICANT: Roberts, TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08
FILING DATE: 09-AUG-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Xu, Tao
                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: David E. Brook
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: BU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07 FILING DATE: 01-NOV-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08
FILING DATE: 28-OCT-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                               INFORMATION:
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                                              Oppenheim, Frank G.
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ilarity 100.0%;
Conservative
                                   Xu, Tao
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F. Donald
ANTI-FUNGAL AND ANTI-BACTERIAL
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Pred. No. 2
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RESULT 4
US-08-485-273A-2
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Patent No.
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Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                       GENERAL INFORMATION:
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                 TITLE OF INVENTION: D-Amino Acid
TITLE OF INVENTION: Anti-Fungal
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 1: MOLECULE TYPE:
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TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                              STATE:
                                                                                            CITY:
                                                                                                      STREET:
                                                                                                                      ADDRESSEE:
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    Application US/08485273A
    5646119

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                                                                                       Lexington
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                                                                                                     E: Hamilton, Brook, Smith & Reynolds, P.C. Two Militia Drive
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
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                                                                                                                                                           D-Amino Acid Histatin-Based Peptides as Anti-Fungal and Anti-Bacterial Agents
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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Pred. No. 28;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     tent No.
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LENGTH: 27 amino acids
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ATTORNEY/AGENT INFORMATION:
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                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                         CORRESPONDENCE
                                                                                                                                                                                                                                                       NPPLICANT: Friden, Philip M.
PITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
PITLE OF INVENTION: Peptides
                                                                                                                                                                                                                                                                                                                         PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/287,717 FILING DATE: 09-AUG-1994
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SOFTWARE: Patent
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                                                                                                                                                        STREET: Two Mil
CITY: Lexington
STATE: MA
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                                                                                                                           COUNTRY: U
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OR APPLICATION DATA:

PLICATION NUMBER.
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                PPLICATION NUMBER:
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07-JUN-1996
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n Release #1.0, Version #1.30
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               US/08/973,563A
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US-08-973-559-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 27 amino acids
                                             FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,888
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
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FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SPACCIAPOLI, PETER
APPLICANT: FRIDEN, PHILIP M.
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
TITLE OF INVENTION: Histatin-Based Peptides
REFERENCE/DOCKET NUMBER: PER95-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Region
                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                   APPLICATION NUMBER: US/08/973,559 FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                      Floppy disk
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RESULT 8
US-08-287-717-9
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                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08287717 Patent No. 5486503
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Patent No. 6555650
GENERAL INFORMATION:
APPLICANT: Lajoie, Gilles A.
TITLE OF INVENTION: Cyclic Analogs of Histatins
FILE REFERENCE: 36555-0002
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Best Local :
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Best Local
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APPLICANT: Oppenh
APPLICANT: Xu, Ta
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PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/693,822B CURRENT FILING DATE: 2000-10-23
                                 ZIP: 0441/
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
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               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                   COUNTRY:
                                                                                                                                                              ADDRESSEE: Hamilton, Brook, STREET: Two Militia Drive
   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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TOPOLOGY: 11
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Xu, Tao
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ilarity 100.0%;
Conservative (
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US/08/287,717
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Pred. No.
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Pred. No.
                                                                                                                                                                            Smith & Reynolds, P.C
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US-08-481-888A-1
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                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/287,717
FILING DATE: 09-AUG-1994
PRIOR APPLICATION DATA:
           REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                         APPLICATION NUMBER: US 08/145,030
FILING DATE: 28-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/786,571
FILING DATE: 01-NOV-1991
                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel
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                                                                                        ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ATTORNEY/AGENT INFORMATION:
NAME: Granabro
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
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APPLICATION NUMBER:
                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Hamilton,
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                                                                           Brook, David E.
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Two Militia Drive
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617-861-9540
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                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.30
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SYSTEM: PC-DOS/MS-DOS
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                                                          22,592
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SEQUENCE CHARACTERISTICS: LENGTH: 38 amino acids

STRANDEDNESS:

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amino acid

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Best Local Similarity 100.0%;
Matches 4; Conservative 0
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                                                                                                                           TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/145,030
FILING DATE: 28-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/786,571
FILING DATE: 01-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
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                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
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                            TOPOLOGY: 11
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OTHER INFORMATION: /product-
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CITY: Lexington
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 09-AUC
                                                          STRANDEDNESS
NAME/KEY: Modified-site
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                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                         NAME: Brook, David E.
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                                                                                          ENGTH:
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07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                     09-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D-Amino Acid Histatin-Based Peptides as Anti-Fungal and Anti-Bacterial Agents
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Pred. No.
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Best Local Similarity
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APPLICATION NUMBER: 08/1
FILING DATE: 28-0CT-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/7
FILING DATE: 01-NOV-91
                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08,
FILING DATE: 09-AUG-94
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CURRENT APPLICATION DATA:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Massachusetts
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    Conservative
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100.0%; Pr
100.0%; Pr
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                   Score 26;
Pred. No.
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                     DB 1; Length 38; 39;
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RESULT 13
US-08-973-559-1
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US-08-973-563A-1
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PRIOR APPLICATION DATA:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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tive 0; Mismatcl
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must have a D configuration."
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                                                                 GENERAL INFORMATION:
APPLICANT: Lajoie, Gilles A.
APPLICANT: Lajoie, Gilles A.
TITLE OF INVENTION: Cyclic Analogs of Histatins
FILE REFERENCE: 36555-0002
CURRENT APPLICATION NUMBER: US/09/693, 822B
CURRENT FILING DATE: 2000-0-23
CURRENT FILING DATE: 2000-10-23
                                                                                                                                                                           Sequence 28, Application US/09693822B Patent No. 6555650
SOFTWARE: PatentIn version 3.1 SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                              PRIOR APPLICATION NUMBER: CA 2,285,673 PRIOR FILING DATE: 1999-10-21 NUMBER OF SEQ ID NOS: 40
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                      Length 38;
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ATTORNEY, AGENT INFORMATION:

NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 anino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-189-331-143
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FEATURE:
INAME/KEY: misc_feature
LOCATION: (2)..(2)
OTHER INFORMATION: phosphoserine
US-09-693-822B-28
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Search completed: August 20, 2003, 12:44:21 Job time: 3.77108 secs
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US-08-189-331-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 143, Application US/08189331
PATENT NO. 5747334
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
                                                                                                                                                   Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/189,331
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
CURSSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 38
TYPE: PRT
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1155 Avenue of the Americas
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Pred. No.
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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121.698 Million cell updates/sec
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:/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep: *
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:/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep: *
:/cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep: *
:/cgn2_6/ptodata/1/pubpaa/US10R_PUBCOMB.pep: *
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  1 US-09-300-425B-31

0 US-09-912-72A-10

1 US-09-880-748-2262

5 US-10-106-698-8476

1 US-09-759-130B-426

4 US-10-042-431-56

US-09-864-761-46278

US-09-739-254-88

US-09-904-615-88

2 US-10-055-098-88

5 US-10-055-098-88

5 US-10-054-988-88

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1 US-09-895-298-161

1 US-09-895-398-163

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1 US-09-764-887-237
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Sequence 31, Appl
Sequence 262, App
Sequence 8476, App
Sequence 426, App
Sequence 56, Appl
Sequence 46278, A
Sequence 88, Appl
Sequence 88, Appl
Sequence 88, Appl
Sequence 88, Appl
Sequence 439, App
Sequence 439, App
Sequence 237, App
Sequence 237, App
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·	US-10-175-737-126	-10-176-758-	-10-174-590-	US-10-052-586-126	-10-194-457	-10-	-172	US-09-876-997-356	-10-199-672-	-10-006-1307	-10-015-387A-	-946-	us-09-731-872-356	US-09-765-205-4	-10	US-09-988-067B-62	US-09-809-391-565	US-10-092-154-972	US-09-764-847-972	US-09-811-284-188	-09-867-5	US-09-815-242-11560	US-09-815-242-11401	US-10-036-542-61	US-10-011-585A-176	ò	6-698	-925-301-1	-09-764-877-	US-09-764-891-4300
	Sequence 126, App	Sequence 126, App		126,	126,	12	8		126	8		ω,	Sequence 356, App	Sequence 4, Appli	ω	σ	565,	972,	•	_	198,		11401	Sequence 61, Appl	176,	108,	Sequence 5417, Ap	$\vdash$	1056	Sequence 4300, Ap

#### ALIGNMENTS

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SEQ ID NO 31
LENGTH: 4
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/09300425B Publication No. US20030045681A1
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGIGGENESIS FILE REFERENCE: SCH-1739P1 CURRENT APPLICATION NUMBER: US/09/300,425B CURRENT FILING DATE: 1999-04-28 DEFICE REPRESENT FILING DATE: 1999-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VITI, Francesca
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B OTHER INFORMATION: antibody clone
                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                         TYPE: PRT
                                  1 FPFY 4
                                                                                        Similarity
                                                                                                                                                                                                                                                                                             PatentIn Ver. 2.1
   FPFY 4
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                                                                         Conservative
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                                                                                          100.0%;
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4.4e+05;
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RESULT

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US-09-912-672A-10

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                                                                                                          RESULT 4
US-10-106-698-8476
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                                     Sequence 8476, Application US/10106698 Publication No. US20030109690A1 GENERAL INFORMATION:
APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/912,672A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/475,541
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication No.
                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
BETOR ETITIN NUMBER: 60/212,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ruben et al. TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. US20020164689A1
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: CLASS II CYTOKINE RECEPTOR-LIKE PROTEINS
TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 07334-184001
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      RIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/
FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/277,379 FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/240,816
FILING DATE: 2000-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION
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et al.
ON: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
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)S: 3239
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Pred. No.
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US-09-759-130B-426
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LENGTH: 22
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Best Local
                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/759,130B CURRENT FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,
TITLE OF INVENTION: USES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/106,69
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/578,063 PRIOR FILING DATE: 2000-05-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE LOCATION: (19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE: MPI00-5350MNIM
                                                                                         APPLICATION NUMBER: US 09/608,452 FILING DATE: 2000-06-30
                                                                                                                                APPLICATION NUMBER: US 09/342,364 FILING DATE: 1999-06-29
                                                                                                                                                                     APPLICATION NUMBER: US 09/596,194 FILING DATE: 2000-07-14
                                                                       APPLICATION NUMBER: US 09/393,996
                                                                                                                                                                                                          FILING DATE: 1999-06-14
                                                                                                                                                                                                                           APPLICATION NUMBER:
                                    APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kirst, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sharp, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodearl, Andrew
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                                                      1999-09-10
                 2000-06-23
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                                    09/602,871
09/420,707
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Pred. No.
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PRIOR FILING DATE: 2000-10-04

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US-09-759-1308-426
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; ORGANISM: Homo sapiens
US-10-042-431-56
         FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
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Best Local Similarity 100.
The Conservative
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SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 426
LENGTH: 23
TYPE: PRT
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SEQ ID NO 56
LENGTH: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
TITLE OF INVENTYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/042,431
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
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TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
                                                                                                                                                                          APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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NUMBER: GB 24263.6
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US-09-864-761-46278
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US-09-739-254-88
; Sequence 88, Application US/09739254
; natent No. US20010021700A1
            COURRENT APPLICATION NUMBER: US/09/739,254
CURRENT FILING DATE: 2000-12-19
EARLIER APPLICATION NUMBER: 09/511,554
EARLIER APPLICATION NUMBER: 09/511,554
EARLIER APPLICATION NUMBER: PCT/US99/1930
EARLIER APPLICATION NUMBER: PCT/US99/1930
EARLIER FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 60/097,917
EARLIER FILING DATE: 1998-08-25
EARLIER FILING DATE: 1998-08-31
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin Ver. 2.0
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SEQ ID
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                                                                                                                                                                                                                                                        TITLE OF INVENTION: 49 Human Secreted Proteins FILE REFERENCE: PZ032P1
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                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
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EXPRESSED IN PLACEN
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IN PLACENTA, SIGNAL - 1.4
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Pred. No. 88;
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; OTHER INFORMATION:
US-09-739-254-88
                                                                                                               Sequence 88, Applica Publication No. US20 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: P2032P1
CURRENT APPLICATION NUMBER: US/10/055,098
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: EARLIER FILING DATE: 2000-02-23
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Patent No. US20020026040A1
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PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/097,917
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NUMBER OF SEQ ID NOS: 170
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TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (47)
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LOCATION: (34)
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LOCATION: (47)
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OTHER INFORMATION: Xaa
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ORGANISM: Homo sapiens
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: LOCATION: (47)
: OTHER INFORMATION: Xaa equals stop translation
US-10-055-098-88
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SEQ ID NO 88
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PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
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SOFTWARE: PatentIn Ver.
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CURRENT FILING DATE: 2002-01-25
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TYPE: PRT
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TITLE OF INVENTION: 49 Human Secreted Proteins
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NAME/KEY: SITE
LOCATION: (34)
OTHER INFORMATION: Xaa
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TYPE: PRT
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Pred. No. 1e+02;
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US-09-895-298-161

Sequence 161, Applic Publication No. US20 GENERAL INFORMATION:

Application US/09895298 b. US20030078405A1

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Query Match
Best Local Similarity
Watches 4; Conserv
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NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 439
LENGTH: 53
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US-09-764-887-237
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Sequence 237, Application US/09764887
Patent No. US200200420998A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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CURRENT FILING DATE: 2001-07-02
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TITLE OF INVENTION: 47
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TYPE: PRT
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SEQ ID NO 237
LENGTH: 68
TYPE: PRT
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Best Local
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior application data removed - NUMBER OF SEQ ID NOS: 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PA113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/073,961
CURRENT FILING DATE: 2002-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-01-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/764,887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE LOCATION: (63)
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OR APPLICATION NUMBER: 60/225,270
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/251,869
OR FILING DATE: 2000-12-08
OR APPLICATION NUMBER: 60/235,834
OR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                       APPLICATION NUMBER: 60/225,757
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/226,868
FILING DATE: 2000-08-22
APPLICATION NUMBER: 60/216,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/217,487 FILING DATE: 2000-07-11 APPLICATION NUMBER: 60/225,758 FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/180,628 FILING DATE: 2000-02-04 APPLICATION NUMBER: 60/214,886 FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/218,290
FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/220,963 FILING DATE: 2000-07-26 APPLICATION NUMBER: 60/217,496 FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/179,065
                                                                                                                                                     APPLICATION NUMBER: 60/225,267 FILING DATE: 2000-08-14
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D. US20030077602A1
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Pred. No. 1.5e+02;
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APPLICATION NUMBER: 60/234,223 FILING DATE: 2000-09-21

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OR APPLICATION NUMBER: 60/22, 514
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OR APPLICATION NUMBER: 60/25, 568
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/25, 368
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OR APPLICATION NUMBER: 60/25, 345
OR APPLICATION NUMBER: 60/23, 370
OR APPLICATION NUMBER: 60/23, 935
OR APPLICATION NUMBER: 60/24, 740
OR APPLICATIO

õ Search completed: August 20, 2003, 13:16:46 Job time : 4.33735 secs 밁 PRIOR APPLICATION NUMBER: 60/241,786
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08 Query Match 100.0%; Score 26; DB 15; Length 68; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels 1 FPFY 4 |||| 65 FPFY 68 0; Gaps 0;

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Title:
Perfect score:
Sequence:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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   26
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Match Length
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-300-425B-31
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30, 30, 30,	000004000414000 70000070404040	sequence 13, sequence 226, sequence 226, sequence 226 sequence 226 sequence 6, sequence 6, sequence 6, sequence 846, sequence 856, sequence 85	Sequence 31, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 86, Appl Sequence 86, Appl Sequence 86, Appl Sequence 86, Appl Sequence 86, Appl Sequence 86, Appl Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl

## ALIGNMENTS

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RESULT 1

US-09-075-338C-31.

Sequence 31, Application US/09075338C

Sequence 31, Application US/09075338C

GENERAL IMPORMATION:

APPLICANT: NERI, Dario

APPLICANT: TARLI, Lorenzo

APPLICANT: VITI, Francesca

APPLICANT: BIRCHLER, Manfred

TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY

FILE REFERENCE: SCH-1773

CURRENT-APPLICATION NUMBER: US/09/075,338C

CURRENT FILING DATE: 1998-05-11

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.1

SOLUTION: APPLICATION OF SEQ ID NOS: 34

CURRENT: APPLICATION OF SEQ ID NOS: 34

CURRENT FILING DATE: 1998-05-11

SOLUTION: APPLICATION OF SEQ ID NOS: 34

CURRENT: APPLICATION OF SEQ ID NOS: 34

CURRENT APPLICATION: Description of Artificial Sequence: anti-ED-B

OTHER INFORMATION: antibody clone

US-09-075-338C-31

Query Match

Best Local Similarity 100.0%; Score 26; DB 14; Length 4;

Best Local Similarity 100.0%; Pred. No. 5.1e+06;
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-512-082-31
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Query Match
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SEQ ID NO 31
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                                                                                                                                                                                                         CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 09/300,425
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                        FILE REFERENCE: SCH-1733P2
CURRENT APPLICATION NUMBER: US/09/512,082
CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                   APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ANGIGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEC ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SPECIFIC BINITITLE OF INVENTION: CONTAINING THE TITLE OF INVENTION: ANGIOGENESIS FILE REFERENCE: SCH-1733P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-300-425B-31
                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B OTHER INFORMATION: antibody clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                              ENGTH:
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                                                                                                                                                                            PatentIn Ver. 2.1
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VITI, Francesca
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                                                         Description of Artificial Sequence: anti-ED-B antibody clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
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Pred. No. 5.1e+06;
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          26;
          DВ
          19;
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                                                                                     RESULT 6
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US-09-224-669-10
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Best Local (
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Best Local
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TYPE: PRT
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US-09-475-541-10

Sequence 10, Application US/09475541

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: CLASS II CYTOKINE RECEPTOR-LIKE PROTEINS
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
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APPLICANT: Busfield, Samantha J.
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APPLICANT: 11ag, Leodevico L.
APPLICANT: 11ag, Leodevico L.
APPLICANT: Ng, Jocelyn, H.
TITLE OF INVENTION: Method for Modifying and Identifying
TITLE OF INVENTION: Functional Sites in Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/224,669
CURRENT FILING DATE: 1998-12-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CLASS II CYTOKINE RECEPTOR-LIKE PROTEINS AND NUCLEIC ACIDS TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: DE 19854196.1 PRIOR FILING DATE: 1998-11-24
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CURRENT FILING DATE: 2001-05-18
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pred. No. 4.5e+02;
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Pred. No.
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5.1e+06;
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CURRENT APPLICATION NUMBER: US/09/475,541
CURRENT FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: U9/224,669
PRIOR FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 10
TYPE: PAT
ORGANITATION
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US-09-475-541-10
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US-09-856-285-10
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GENERAL INFORMATION:
APPLICANT: 1lag, Leodevico L.
APPLICANT: Ng, Jocelyn, H.
TITLE OF INVENTION: Method for Modifying and Identifying
TITLE OF INVENTION: Functional Sites in Proteins
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Best Local S
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GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
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                   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 10
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/856,285
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: PCT/EP99/09052
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: DE 19854196.1
PRIOR FILING DATE: 1998-11-24
                                                                                                                  TITLE OF INVENTION: CLASS II CYTOKINE RECEPTOR-LIKE PROTEINS TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THEM FILE REFERENCE: 0734-184001
CURRENT APPLICATION NUMBER: US/09/912,672
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/475,541
PRIOR EPLICATION NUMBER: 09/475,541
PRIOR EPLING DATE: 1998-12-31
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                   NUMBER OF SEQ ID NOS:
ORGANISM: Homo sapiens
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nilarity 100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-856-285-11
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: Busfield,
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Best Local :
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TYPE: PRT
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Pred. No. 4.5
); Mismatches
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Pred. No.
                                                                                                                                                         Score 26;
Pred. No.
                                                                                                                            DB 23;
4.9e+02;
hes 0;
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RESULT 11

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US-07-867-819A-86
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                                                                                                                                                                                                   Sequence 86, Application US/07867819A GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Relaction DATA:
CURRENT APPLICATION NUMBER: US,
FILING DATE: 13-APR-199
                                                                                                                                                                                    APPLICANT:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/472,947 FILING DATE: 31-JAN-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                            COUNTRY: USA
ZIP: 30309-3450
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                                                                                            STREET:
                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                     Local
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REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 30309-4530
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amino acid
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                                                                                       2800 One-Atlantic Center, 1250 West Peachtree Street
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1100 Peachtree Street
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                                                                                                       Patrea L. Pabst
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                                                                                                                                                   METHODS AND REAGENTS FOR DIAGNOSIS OF AUTOANTIBODIES
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Pred. No. 5
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US-07-867-819B-86
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                                                           Matches
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Best Local (
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                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 122 SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
PRIOR APPLICATION NUMBER: 07/648,205
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/07/867,819B CURRENT FILING DATE: 1992-04-13
                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Harley, John TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies FILE REFERENCE: OMRF 114 CIP (2)
                                                                                                                                  LOCATION: (4)..(11)
OTHER INFORMATION: Binding site
                                                                                                                                                                                               TYPE: PRT
ORGANISM: homo sapien
                                                                                                                                                               NAME/KEY: MISC_FEATURE
                                                                                                                                                                                    FEATURE:
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LENGTH: 12 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
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CURRENT APPLICATION DATA:
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                                                         Similarity 4; Conserv
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31-JAN-1990
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Pred. No.
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; NAME/KEY: MISC_FEATURE
; LOCATION: (4). (11)
; OTHER INFORMATION: Binding site
US-07-867-819D-86
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US-08-475-955-86
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LENGTH: 12
TYPE: PRT
ORGANISM: homo sapien
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GENERAL INFORMATION:
APPLICANT: Harley, John
APPLICANT: Harley, John
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
FILE REFERENCE: OMRF 114 CIP (2)
CURRENT APPLICATION NUMBER: US/07/867,819D
CURRENT FILING DATE: 1992-04-13
PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
PRIOR FILING DATE: 1990-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 86, Applications
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Best Local :
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PRIOR FILING DATE: 1991-01-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin version 3.1
                                                                                                                                                   APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: APrll 13, 1992
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
APPLICATION NUMBER: 07/472,947 FILING DATE: January 31, 1990 ATTORNEY/AGENT INFORMATION:
                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 100.0%; Score 26; DB 3; Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0;
                                                                              APPLICATION NUMBER: 07/648,205 FILING DATE: January 31, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Atlanta
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2800 One Atlantic Center, 1250 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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Search completed: August 20, 2003, 13:13:42 
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                                                                                             Best Loc
Matches
                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: OM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                 FEATURE:
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nes 4; Conserv
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LOCATION:
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                                                                                              Score 26; DB 8;
Pred. No. 5.3e+02;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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length: 2000000000
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1 FPFY 4
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| Cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
| Cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
| Cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
| Cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
| Cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
| Cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
| Cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
| Cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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US-10-376-121A-86
US-10-673-573-8043
US-10-612-783-4565
US-10-603-113-25825
US-10-603-113-27267
US-10-603-113-27267
US-10-617-320-3303
US-10-617-330-3203
US-10-612-783-5205
US-10-612-783-5205
US-10-612-783-5216
US-10-612-783-5219
US-10-612-783-6421
US-10-612-783-6421
US-10-612-783-6421
US-10-612-783-6421
US-10-612-783-6421
US-10-612-783-6421
US-10-612-783-6380
US-10-612-783-6380
US-10-612-783-4817
US-10-286-897-1962
US-10-286-897-1962
US-10-633-113-19356
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Sequence
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886, Appl
4565, Ap
25825, A
23128, Ap
271267, A
271267, Ap
271267, Ap
27126, Ap
27127, Ap
27127,
                                                                  MOLECULE TYPE: FEATURE:
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## ALIGNMENTS

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RESULT 1

US-10-376-121A-86

US-10-376-121A-86

Sequence 86, Application US/10376121A

Sequence 86, Application US/10376121A

Sequence 86, Application:

APPLICANT: Harley, John

TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF

NUMBER OF SEQUENCES: 218

CORPESPONDENCE ADDRESS:

ADDRESSSE: Patrea L. Pabst

STATE: GA.

COUNTRY: USA

COMPUTER: Suite 2000, 1201 West Peachtree Street, N.E.

CITY: Atlanta

STATE: GA.

COMPUTER: USA

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patrentin Release #1.0, Version #1.25

COMPUTER: IBM PC COMPATION SOFTWARE: PAPPLICATION NOTA:

APPLICATION NUMBER: US/10/376,121A

FILING DATE: JT-Mar-2003

CLASSFICATION UNMBER: US/10/376,121A

FILING DATE: JT-Mar-2003

CLASSFICATION UNMBER: 07/867,819

FILING DATE: JANUARY 31, 1991

APPLICATION NUMBER: 07/867,819

APPLICATION NUMBER: 07/867,819

FILING DATE: JANUARY 31, 1991

APPLICATION NUMBER: 07/867,819

APPLICATION NUMBER: 07/867,819
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RESULT 4
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                                                                                                                                                Query Match
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/612,783
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53373)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                             ENGTH: 59
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Pred. No. 14;
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Pred. No. 5
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                                                                                                                                 DB 6; Length 59; 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Candida albicans US-10-603-113-23128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Candida albicans US-10-603-113-25825
GRGANISM: Candida albicans US-10-603-113-27267
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                                                                                                                                                                                                     Sequence 27267, Application US/10603113
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: UCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/603,113
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 23128
LENGTH: 67
                                                                               SEQ ID NO 27267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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LENGTH: 62
TYPE: PRT
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Best Local
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                                                                                                  PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/603,113
CURRENT FILING DATE: 2003-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBITITED OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/10/603,113
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PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
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                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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Pred. No.
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Pred. No.
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NAME/KEY: misc_feature;
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LOCATION: (B) LOCATION 1...75
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SEQUENCE DESCRIPTION: SEQ ID NO: 3303:
US-10-617-320-3303
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                        TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3303:
SEQUENCE CHARACTERISTICS:
                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/617,320 FILING DATE: 10-Jul-2003 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                             MOLECULE TYPE: protein
39
                              1 FPFY 4
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OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60,08131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60,051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
 FPFY 42
                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                           ENGTH:
                                                         100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                           75 amino acids
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                                                                                                                                                                                                  Streptococcus
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Pred. No. 26;
                                                                           Score 26; DB Pred. No. 29;
                                                            Mismatches
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RESULT 8

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; ORGANISM: Candida albicans US-10-603-113-27139
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US-10-612-783-5205
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US-10-603-114-8012
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
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SEQ ID NO 27139
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SEQ ID NO 8012
LENGTH: 77
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
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CURRENT APPLICATION NUMBER: US/10/603,114
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/543,681
PRIOR FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
                                CURRENT APPLICATION NUMBER: US/10/612,783
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
                                                                                          APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53373)A
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                                                                                                                                                                                      APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR FILING DATE: 1999-04-09
                                                                                                                                                      APPLICANT:
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TYPE: PRT
Q ID NO 5205
LENGTH: 80
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nilarity 100.0%;
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Pred. No.
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                                                                                                                                  And Other Molecules Associated With
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; OTHER INFORMATION:
US-10-631-402-2116
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; CARANISH: Zea mays;
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4577_179465C.1.pep
US-10-612-783-5205
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US-10-631-402-2116
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                                                                                  Query Match
Best Local Similarity
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SEQ ID NO 2116
LENGTH: 94
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 08/905,133
PRIOR FILING DATE: 1997-08-01
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CURRENT FILING DATE: 2003-07-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 3475
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PRIOR FILING DATE: 2000-04-11
                                                                                                                                                                                  NAME/KEY: UNSURE
                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                                                            NAME/KEY: SIGNAL LOCATION: -24.'.-1 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Hypertrophic prostate
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPPLICANT: Dumas Milne Edwards, Jean Baptiste
                                                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1997-08-01
APPLICATION NUMBER: US 08/905,279
FILING DATE: 1997-08-01
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APPLICATION NUMBER: US 08/905,135
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APPLICATION NUMBER: US 08/905,051
FILING DATE: 1997-08-01
      54 FPFY 57
                                      1 FPFY 4
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Lacroix, Bruno
                                                                   Conservative
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                                                                                                                                                                                                                                                score 6.60
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                                                                Score 26; DB Pred. No. 35; Mismatches
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Pred. No.
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Best Local Similarity
"~+~hes 4; Conserva
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                                                                                                                           Sequence 5529, Application US/10612783 GENERAL INFORMATION:
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SEQ ID NO 2116
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               APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
                                                                      APPLICANT:
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CURRENT FILING DATE: 2003-07-30
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PRIOR FILING DATE: 1997-08-01
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PRIOR FILING DATE: 2000-04-11
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NITLE OF INVENTION: Expressed Sequence Tags
FILE REFERENCE: GEN-T119C1
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: UNSURE LOCATION: 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
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REFERENCE:
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                                      Zhou, III.
                                                                                                        La Rosa, Thomas
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                                                                                         Kovalic, David
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APPLICANT: Wong, James F. H.

TITLE OF INVENTION: Orally Active Pesticidal Biopeptides
FILE REFERENCE: 35718/260673

CURRENT APPLICATION NUMBER: US/10/617,978

CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: 60/395,428
PRIOR APPLICATION NUMBER: 60/395,428
PRIOR FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 103
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
FEATURE:
TYPE: PRT
ORGANISM: Artificial Sequence
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                 Sequence 576, Application US/10612783

SEQUENCE 576, Application US/10612783

SEQUENCE 576, Application:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53373)A

CURRENT APPLICATION NUMBER: US/10/612,783

CURRENT FILING DATE: 2003-07-02
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SEQ ID NO 5576
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CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
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LENGTH: 99
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Search completed: August 20, 2003, 12:45:14 Job time: 2.15663 secs
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NAME/KEY: unsure
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OTHER INFORMATION: un
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Title: Perfect score: Sequence:

9

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                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <KUR>
A;Cross-references: GB:
C;Genetics:
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                                                                                                                    RiShe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redd arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: D90403
                                                                                                                                                                                                                          hypothetical protein SSO10228 [imported] - Sulfolobus solfataricus transposon ISC1058 C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: D90403
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A;Residues: 1-45 <HEI-A
A;Residues: 1-45 HEI-A
A;Cross-references: GB:AE004284; GB:AE003852; NID:g9656649; PIDN:AAF95248.1; GSPDB:GN
A;Experimental source: serogroup O1; strain N16961; blotype E1 Tor
C;Genetics:
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A; Map position: 1
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Risabatini, L.M.; Azen, E.A.

Blochem. Blophys. Res. Commun. 160, 495-502, 1989

Blochem. Histatins, a family of salivary histidine-rich

A; Reference number: A90156; MUID:89246491; PMID:2719677

A; Accession: A32541
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-2000
C;Accession: 157425; A32541; A32987; A25661; A60664; A28164; A60742; A60659
R;Sabatini, L.M.; Ota, T.; Azen, E.A.
Mol. Biol. Evol. 10, 497-511, 1993
A;Title: Nucleotide sequence analysis of the human salivary protein genes HI A;Reference number: 157425; MUID:93330039; PMID:8336540
A;Accession: 157425
                      R; vanderSpek, J.C.; Offner, G.D.; Troxler, R.F.; Oppenheim, Arch. Oral Biol. 35, 137-143, 1990
A; Title: Molecular cloning of human submandibular histatins A; Reference number: A60659; MUID:90262442; PMID:2344289
                                                                                                                                                                  J. Dent. Res. 69, 2-6, 1990
A;Title: Structural relationship between human salivary
A;Reference number: A60742; MUID:90154430; PMID:2303595
A;Accession: A60742
                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 20-57 <SUS
R;Oppenheim, F.G.; Xu, T.; McMillian, F.M.; Levitz, S.M.; Diamond
J. Biol. Chem. 263, 7472-7477, 1988
A;Title: Histatins, a novel family of histidine-rich proteins in
A;Reference number: A94685; MUID:88227937; PMID:3286634
                                                                                                                   A; Molecule type: protein A; Residues: 31-57 < TRO>
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A; Residues: 20-57 < OP2>
R; Troxler, R.F.; Offner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 20-57 <0Pp. A;Rich. Oral Biol. 35, 415-419, 1990
A;Title: Rapid purification and characterization of histatins (histidine-rich polypepti A;Reference number: A60664; MUID:90321151; PMID:2372245
A;Accession: A60664
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A;Residues: 14-57 <VANA
R;Oppenheim, F.G.; Yang, Y.C.; Diamond, R.D.; Hyslop, D.; Offner,
J. Biol. Chem. 261, 1177-1182, 1986
A;Title: The primary structure and functional characterization of
A;Reference number: A25661; MUID:86111755; PMID:3944083
A;Accession: A25661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M26664; NID:g292143; PIDN:AAA58645.1; PID:g292144 R;VanderSpek, J.C.; Wyandt, H.E.; Skare, J.C.; Milunsky, A.; Oppenheim, F. Am. J. Hum. Genet. 45, 381-387, 1989 A;Title: Localization of the genes for histatins to human chromosome 4q13 A;Reference number: A32987; MUID:89371745; PMID:2773933 A;Accession: A32987
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A; Residues: 1-57 <SA
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A; Residues: 1-57 <SAB>
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                                                                                                                                                                                                                                                             G.D.; Xu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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; Mismatches
                                                                                                                                                                                                                                                          T.; Vanderspek, J.C.; Oppenheim,
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Oppenheim, F.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                            G.D.;
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                                                                                                                                                                                               R;Gattung; S. submitted to the EMBL Data Library, Februa submitted to the sequence of C. elegans
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A; Residues: 'VML', 14-57 <VA2>
C; Genetics:
                                                                                                                                                                                                                                                                                   hypothetical protein K10B3.1 - Cac
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_rev
C;Accession: T16615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete,
A; Reference number: A/0100; MUID:98065943; PMID:9403685
A; Accession: C70246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein BBJ10 - Lyme disease spirochete plasmid J/lp38 C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 C;Accession: C70246
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A; Introns: 17/3; 24/3; 34/3
C; Superfamily: histatin precursor;
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                                                                                        A; Molecule type: DNA
A; Residues: 1-73 <GAT>
                                                                                                                                                             A; Accession:
                                                                                                                                                                                     A; Description: The sequence A; Reference number: Z18546
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A; Residues: 1-68 < KLE>
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                                            A; Experimental
                                                                    A; Cross-references:
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                                         EMBL:U49941; NID:g1206038; PID:g1206042; ce: strain Bristol N2; clone K10B3
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ce: strain B31
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                                                                    PIDN:AAB53870.1; GSPDB:G
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PID:g2690189;

burgdorferi.

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C;Genetics:
A;Gene: GDB:FKHL10; FREAC6
A;Cross-references: GDB:4502
A;Map position: 5q34 5q34
C;Superfamily: unassigned fc
F;6-76/Domain: fork head DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FREAC-6 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1999
C;Accession: S51629
R;Pierrou, S.; Hellqvist, M.; Samuelsson, L.; Enerbaeck, S.; Carlsson, P.
EMBO J. 13, 5002-5012, 1994
A;Title: Cloning and characterization of seven human forkhead proteins: bind A;Reference number: S51624; MUID:95045392; PMID:7957066
A;Accession: S51629
A;Status: preliminary; nucleic acid sequence not shown
A;Mesidues: 1-76 <PIE>
A;Cross-references: EMBL:U13224; NID:g563167; PIDN:AAA92041.1; PID:g563168
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A; Introns: 25/3
                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 - KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73598.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asr1899
                                                                                                                                                                                                                 A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AE2043
                                                                                                                                                                                                                                                                                                           hypothetical protein asr1899 [imported] - Nostoc sp. (strain PCC C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. s C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 0 C;Accession: AE2043
                                                                                                                                                                                                                                                Nakazaki, N.; Shimpo, S.;
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
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ilarity 100.0%;
Conservative (
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, M.; Yasuda, N
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09-Dec-2002
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awa: Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; The arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: A99427
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: E90483
                                                                                                                                                                     RESULT 10
C56556
C56556
fork head homolog XFD-2' - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 31-Oct-1997
C;Accession: C56556
C;Accession: C56556
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A; Residues: 1-92 < KUR>
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A; Accession: E90483
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C; Species: Sulfolobus solfataricus
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                                                            A; Title: Activin A induced expression of a A; Reference number: A56556; MUID: 93041288; A; Accession: C56556
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A; Residues: 1-97 < KUR>
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C; Species: Sulfolobus solfataricus
A; Molecule type: mRNA
A; Residues: 1-97 < KNO>
                                                                                                                               R; Knochel, S.; Lef, J.; Clement, Mech. Dev. 38, 157-165, 1992
                                          A; Status: preliminary;
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Best Local Similarity
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                                                                                                                                                     J.; Klocke, B.; Hille, S.;
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Pred. No. 80;
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Pred. No.
                                            with conceptual translation
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                                                                                       fork head related PMID:1358174
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goc, H.P.; Redder
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Redder
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HNF-3/fork-head homolog-3 - human (fragment)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence_revision 10-May-1996 #text_change 12-Sep-1997
C:Accession: A47450
C:Accession: Accession: Accession:
                   brain factor-3 - rat (fragment)
C; Species: Rattus norvegicus (N
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160918
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F; 3-94/Domain:
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A; Residues: 1-101 <RES>
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R;NOLIIng, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Dally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the A;Reference number. A96900; MUID:21359325; PMID:21359325, A;Accession: B96969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-99 < KUR>
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Best Local :
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Pred. No.
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Pred. No.
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A; Residues: 1-105 < KUR>
A; Cross-references: GB:
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R;Clevidence, D.E.; Overdier, D.G.; Tao, W.; Qian, X.; Pani, L.; Lai, Proc. Natl. Acad. Sci. U.S.A. 90, 3948-3952, 1993
A;Title: Identification of nine tissue-specific transcription factors A;Reference number: A47450; MUID:93248207; PMID:7683413
A;Accession: I60919
                                                                                                                                                                             R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Al
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng,
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                  C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: F90335
                                                                                                         A; Reference number: A99139
A; Accession: F90335
                                                                                                                                                                                                                                                                                                                                    hypothetical protein SSO1745 [imported] - C; Species: Sulfolobus solfataricus
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A;Title: Identification of nine tissue-specific transcription fac A;Reference number: A47450; MUID:93248207; PMID:7683413
A;Accession: I60918
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A; Residues: 1-101 <RES>
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
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GB:AE006641; NID:g13814989;
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PRR2_TOBAC
YSV4_CAEEL
LI31_CAEEL
SRY_CAEHI
SRY_SHEEP
Y382_METJA
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TANDARD;  11, Last sequences of the primates;  22 Last annowed and primates;  23 PubMed=27196;  25 PubMed=27196;  25 PubMed=27196;  26 Res. Commun.  27 PubMed=83365;  28 PubMed=83365;  29 PubMed=12477;  20 PubMed=12477;  20 PubMed=12477;  20 PubMed=12477;  21 PubMed=12477;  21 PubMed=12477;  21 PubMed=12477;  22 PubMed=12477;  23 PubMed=12477;  24 PubMed=12477;  25 PubMed=12477;  26 PubMed=12477;  27 PubMed=12477;  28 PubMed=12477;  29 PubMed=12477;  20 PubMed=12477;  20 PubMed=12477;  21 PubMed=12477;  21 PubMed=12477;  21 PubMed=12477;  22 PubMed=12477;  23 PubMed=12477;  24 PubMed=12477;  25 PubMed=12477;  26 PubMed=12477;  27 PubMed=12477;  27 PubMed=12477;  28 PubMed=12477;  29 PubMed=12477;  20 PubMed=12477;  20 PubMed=12477;  21 PubMed=12477;  21 PubMed=12477;  21 PubMed=12477;  22 PubMed=12477;  23 PubMed=12477;  24 PubMed=12477;  25 PubMed=12477;  26 PubMed=12477;  27 PubMed=328667;  27 PubMed=3286		329 329 336 337 347 347 351 351 353 353 353 353
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Sugiyama K., Ogino T., Ogata K.;
"Rapid purification and characterization
polypeptides) from human whole saliva.";
Arch. Oral Biol. 35:415-419(1990).
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tissue distribution of the
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MEDLINE-86111755; PubMed-3944083;
Oppenheim F.G., Yang Y.C., Diamon
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J. Biol. Chem. 263:7472-7477(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Troxler R.F.;
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                                                                                                                                                            G0:0005576; C:extracellular; NAS.
G0:0003797; F:antibacterial peptide activity; NAS.
G0:000952; P:defense response; NAS.
mineralization; Fungicide; Antibiotic; Signal; Phos
                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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PTM: HISTATIN 2 IS A PROTECLYTIC PRODUCT OF HISTATIN 1.

SIMILARITY: TO HISTATIN 3.
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43
                                                                                                                                                                                                                                                                                          M26664; AAA58645.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ization of the genes for histatins distribution of the mRNAs."; Hum. Genet. 45:381-387(1989).
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FPFY
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                                       30-MAY-2000 (Rel. 39, Last sequence update)
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Forkhead box protein C2 (Brain factor-3) (BF-3)
FOXC2 OR HFHBF3.
                              Rattus norvegicus (Rat).
                                                                  Q63246;
30-MAY-2000 (Rel. 39,
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30-MAY-2000 (Rel. 39,
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           Mammalia;
                    Eukaryota; Metazoa;
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Forkhead box
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PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
DNA-binding; Nuclear protein; Transcription
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ProDom; PD000425; TF_Fork_head; 1.
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Pfam; PF00250; Fork_head; 1.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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FOXL2 OR PFRK.
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TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADULT
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Mismatches
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Sciurognathi; Muridae; Murinae; Mus
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhead box protein Il (Forkhead-related protein FKHL10) (Forkhead-related transcription factor 6) (FREAC-6) (Hepatocyte nuclear factor 3 forkhead homolog 5) (HFH-5) (Fragment).
FOXII OR FKHL10 OR FREAC6 OR HFH5.
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ProDom; PD000425; TF_Fork_head; 1.

SMART; SM00339; FF; 1.

PROSITE; PS00659; FORK_HEAD_1; 1.

PROSITE; PS00658; FORK_HEAD_2; 1.

PROSITE; PS0039; FORK_HEAD_3; 1.
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MEDLINE-93248207; PubMed-7683413;
Clevidence D.E., Overdier D.G., Tao
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SEQUENCE FROM N.
                                                                              "Identification of nine tissue-specific transcription for hepatocyte nuclear factor 3/forkhead DNA-binding-domain Proc. Natl. Acad. Sci. U.S.A. 90:3948-3952(1993).
-- SUBCELLULAR LOCATION: Nuclear.
-- SIMILARITY: Contains 1 fork-head domain.
                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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HSSP; Q63245; 2HFH.
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Pfam; PF00250; Fork_head; 1.
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pht. It is produced through a collaboration Bioinformatics and the EMBL outstation
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        EMBL; AE001535; AAD06654.1; PIR; G71851; G71851. HAMAP; MF_00402; -; 1.
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Query Match
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Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                        Q9ZK67;
30-MAY-2000
                                                                                                                                                                                                                                                                                                      PROSITE; PS00657; FORK_HEAD_1; PROSITE; PS00658; FORK_HEAD_2; PROSITE; PS50039; FORK_HEAD_3;
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ProDom; PD000425; TF_Fork_head; 1.
SMART; SM00339; FH; 1.
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TRANSFAC; T102480; -.
InterPro; IPR001766; TF_Fork_head.
Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
  50S ribosomal
               30-MAY-2000
28-FEB-2003
                                                                 RL19_HELPJ
                                                                                                                                                                                                                                        SEQUENCE
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101 AA;
(Rel. 39, Created)
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protein L19.
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                                                                 STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial "Genomic sequence comparison of two unrelated isolates of the hum gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-I- FUNCTION: THIS PROTEIN IS LOCATED AT THE 30S-50S RIBOSOMAL SU INTERPACE AND MAY PLAY A ROLE IN THE STRUCTURE AND FUNCTION O AMINOACYL-TRNA BINDING SITE (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE L19P FAMILY OF RIBOSOMAL PROTEINS. Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G. Tummino P.J., Caruso A., Uria Nickelsen M., Mills D.M., I Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., SEQUENCE FROM N.A. MEDLINE-99120557; PubMed-991205682; Helicobacter pylori J99 (Campylobacter pylori J99). Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter. RPLS OR JHP1074 or send an email to license@isb-sib.ch). entities requires a license agreement (See http://www.isb-sib.ch/announce/ Trust NCBI\_TaxID=85963; Ives C the human Vovis Doig P.C., , SUBUNIT G.F.,

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-26695 / ATCC 700392;

MEDLING-97394467; PubMed-9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Glodek A., Nelson B., Richardson D., Dodson R., Khalak H.G., Glodek A., KritzGerald L.M., Lee N., Adams M.D., Hickey E.K., WcKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., HitzGerald J.M., Fujii C., Bowman C., Watthey L., Wallin E. Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E. Cotton M.D., Weidman J.M., Karp P.D., Smith H.O., Fraser C.M.,
                            PRINTS; PR00061; RIBOSOMALL19; 1. ProDom; PD002979; Ribosomal_L19; 1. TIGRFAMS; TIGR01024; rp1S_bact; 1. PROSITE; PS01015; RIBOSOMAL_L19; 1.
                                                                                      TIGK; HP114/; -.
HAMAP; M=00402; -; 1.
InterPro; IPR001857; Ribosomal_L19.
Pfam; PF01245; Ribosomal_L19; 1.
                                                                                                                                                   PIR; C64663;
                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                pylori.
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                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria;
Helicobacteraceae; Helicobacter.
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01-NOV-1997
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PROSITE; PS01015; RIBOSOMAL_L19; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 118 AA; 13616 MW; 8B21B6
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ProDom; PD002979; Ribosomal_Li
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Pfam; PF01245; Ribosomal_L19; 1.
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                                                                                                                                                                                                                                                                                                  FUNCTION: THIS PROTEIN IS LOCATED AT THE 30S-50S RIBOSOMAL SI INTERFACE AND MAY PLAY A ROLE IN THE STRUCTURE AND FUNCTION (AMINOACYL-TRNA BINDING SITE (BY SIMILARITY).

SIMILARITY: BELONGS TO THE L19P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                    HP1147;
                                                                                                                                                                 AE000621;
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    118 AA;
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                                                                                                                                                C64663
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                Complete proteome
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  13600 MW;
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n; Calcium; Signal.
BY SIMILARITY.
PHOSPHOLIPASE A2 5
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PROSITE; PS00118; PA2\_HIS; PROSITE; PS00119; PA2\_ASP;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000303; Pho
SMART; SM00085; PA2c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF539921; AAN77204.1;
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15-SEP-2003
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Viperidae; Viperinae; E
NCBI_TaxID=99586;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carpet vipers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acylhydrolase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acylelycerophosphocholine + a fatty acid anion.
COFACTOR: Binds 1 calcium ion per subunit (By similarity).
SUBCELLULAR LOCATION: Secreted (By similarity).
TISSUE SPECIFICITY: Expressed by the venom gland.
SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acyl groups in 3-sn-phosphoglycerides (B
CATALYTIC ACTIVITY: phosphatidylcholine
acylglycerophosphocholine + a fatty acid
COFACTOR: Binds 1 calcium ion per subuni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Chordata; Craniata; Vertebra
ata; Scleroglossa; Serpentes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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glycerides (By similarity).
tidylcholine + H(2)0 = 1-
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erpentes; Colubroidea;
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                                                                                                                                                                                        RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA bazevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chim S.Y., Glaser P., Goffeau A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Kurita K., Lapidus A., Eardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror F., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RT The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89155435; PubMed=2537815; Trach K., Hoch J.A.; Trach K., Hoch J.A.; "The Bacillus subtilis spoOB stage 0 essential GTP-binding protein."; J. Bacteriol. 171:1362-1371(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last seq
28-FEB-2003 (Rel. 41, Last ann
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P21204;
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                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                  -|- PATHWAY: L-phenylalanine
                                                                                                                                                                   Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98044033; PubMed=9384377;
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                                        ween the Swiss Institute of Bioinfo
                                                                                                                                            CATALYTIC ACTIVITY:
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                                                                                                        1s.";
390:249-256(1997).
TALYTIC ACTIVITY: Chorismate - prephenate.
T-nhenvlalanine biosynthesis.
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Last annotation update)
Itase (EC 5.4.99.5) (CM)
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Pred. No.
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EMBL; M24537; AAA22506.1;
EMBL; 299118; CAB14751.1;
PIR; D32804; D32804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bauer U., Flunker G., Seidel W.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
1- FUNCTION: FORMS A COMPLEX WITH THE HEAVY CHAIN OF THE CL.
TRANSPLANTATION ANTIGENS DURING AN ADENOVIRUS INFECTION,
REDUCING CLASS I EXPRESSION ON THE CELL SURFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-Human adenovirus type 2;

MEDILINE-81053687; PubMed-6523880;

Herisse J., Courtois G., Galibert F.;

"Nucleotide sequence of the Ecori D f

"Nucleic Acids Res. 8:2173-2192(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E3GL_ADE02 STANDARD; PRT; 159 AA P03251; P03251; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation updat Early E3 18.5 kDa glycoprotein precursor (G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002912; ACT. Pfam; PF01842; ACT; 1. Phenylalanine biosynthesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-Human adenovirus type 6; Reichmann H., Schaarschmidt E., Geisler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human adenovirus type 2, and Human adenovirus type 6. Viruses; dSDNA viruses; no RN NCBI_TaxID=10515, 10534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                    EMBL; J01917; AAA92221.1; EMBL; Y16037; CAA75990.1;
                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: TO OTHER ADENOVIRUSES GP19K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   reticulum.
                                                                                                                                                                                   A03821;
                                                                                                                      protein;
                                                                                                                                         PF04881; Adeno_GP19K;
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Transmembrane; (1) 17 PP 18 159 E. 18 123 L. 18 124 PP 159 C. 29 N
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Pred. No.
  LUMENAL (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .)
                                                                                  EARLY E3
                                                                                                                        Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor (GP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I membrane protein.
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                                                                                  kDa GLYCOPROTEIN
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                                                                                                                          Signal
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Best Local
    CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                   EMBL; M73260; -; NOT_ANNOTATED_CDS.
EMBL; M30002; CAA26783.1; -.
EMBL; M14406; AA442492.1; -.
PIR; A03822; ERADA5.
                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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E3GL_ADE05
P04494;
                                                                          DOMAIN
                                                                                             TRANSMEM
                                                                                                                       DOMAIN
                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                         InterPro; IPR006965; Adeno_GP19K.
Pfam; PF04881; Adeno_GP19K; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chroboczek J., Bieber F., Jacrot B.;
"The sequence of the genome of adenovirus type 5 and its compari with the genome of adenovirus type 2.";
Virology 186:280-285(1992).
-1--EUNCTION: FORMS A COMPLEX WITH THE HEAVY CHAIN OF THE CLASS TRANSPLANTATION ANTIGENS DURING AN ADENOVIRUS INFECTION, THE REDUCING CLASS I EXPRESSION ON THE CELL SURFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Early E3 18.5 kDa glycoprotein precursor (GP19K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=85130985;
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MEDLINE=85092388; PubMed=
Cladaras C., Wold W.S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92087470; PubMed=1727603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLETE GENOME.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "DNA sequence of the early E3 transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID-28285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: TO OTHER ADENOVIRUSES GP19K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINE=85130985; PubMed=3882694;

W.S.M., Cladaras C., Deutscher S.L., Kapoor Q.S.;
e 19-kDa 91ycoprotein coded by region E3 of adenovirus.
ification, characterization, and structural analysis.";
Biol. Chem. 260:2424-2431(1985).
                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
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                  POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...)
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                                                                                                              LUMENAL (POTENTIAL).
                                                                                                                                   EARLY E3 18.5 kDa GLYCOPROTEIN
                                                                                                                                                        POTENTIAL
                                                                                                                                                                             Glycoprotein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26;
Pred. No.
B1F0D2AC4D6330E0 CRC64;
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                  (POTENTIAL).
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ID Y453_HAEIN
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Best Local
      DP1_HUMAN STANDARD; PRT; 185 AA Q00765; Q04198; Q9BWH9; O1-APR-1993 (Rel. 25, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Whole-genome random rand
                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1995
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 269:496-512(1995).
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MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Typothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole-genome random sequencing and assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
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174 AA;
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166
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32, Last sequence update)
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                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                     Score 26; DE
Pred. No. 72;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                             32A2F39303399B48 CRC64;
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RA Strausberg R.D., Felipgold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Chaleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugdin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Althory J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Shevchenko Y., Bouffard G.G.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RG Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences ",
L.-. Sunceri M. A., Schent J. S.A., 99:16899-16903(2002).
                                                                                                                                                             EMBL;
PIR; /
MIM; ]
                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                     Pfam;
                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91335210; PubMed=1651562;
Kinzler K.W., Nilbert M.C., Su L.K., Vogelstein B., Bryan T.M.,
Levy D.B., Smith K.J., Preisinger A.C., Hedge P., McKechnie D.,
Finniear R., Markham A., Groffen J., Boguski M.S., Altschul S.F.,
Horil A.K., Ando H., Miyoshi Y., Miki Y., Nishisho I., Nakamura Y.;
*Identification of FAP locus genes from chromosome 5q21.";
Science 253:661-665(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Joslyn G., Carlson M., Thliveris A., Albertsen H., Gelbe Samowitz W., Groden J., Stevens J., Spirio L., Robertson Sargeant L., Krapcho K., Wolff E., Burt R., Hughes J.P., Warrington J., McPherson J.D., Wasmuth J.J., le Paslier Abderrahim H., Cohen D., Leppert M., White R.; "Identification of deletion mutations and three new gene familial polyposis locus.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-91335210;
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                                                                                                                                        GO:0016021;
                                                                                                                                                                                                                                                                                                                                                                                                                                c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
SUBCELLULAR LOCATION: Integral membrane protein
SIMILARITY: TO C.ELEGANS T19C3.4.
                                                                                                                                                                              ; M73547; AAA60136.1; -. M74090; AAA66351.1; ALT_INIT; BC000232; AAH00232.1; -. A39658; A39658;
                                                                                               O:0016021; C:integral to
Pro; IPR004345; TB2_DP1_
PF03134; TB2_DP1_HVA22;
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159
                                                                                                                 L_HVA22
POTENTIAL.

POTENTIAL.

M -> I (IN

A -> S (IN
                                                                                                                                    membrane;
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REF.
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RESULT 13
RUIA_DROME
ID OI OI -NOV
DT 01 -
RX MEDLING-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Kalchards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berson K.J., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gharty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA George Y.J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Sounge S.M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriera C., Ferriera S., Fleischmann W.,
RA George C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Kraft C., Kez J., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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Best Local
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MEDLINE-95011590; PubMed-7926776;
Flickinger T.W., Salz H.K.;
"The Drosophila sex determination
with sequence and functional simil
protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determination protein SNF).

SNF OR D25 OR LIZ OR FS(1)1621 OR CG4528.

Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Hexapoda, Inse
Neoptera; Endopterygota; Diptera; Brachycera,

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harper D.S., Fresco L.D., Keene J.D.; "RNA binding specificity of a Drosophila snRNP protein that shares sequence homology with mammalian U1-A and U2-B' proteins."; nucleic Acids Res. 20:3645-3650(1992).
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P43332; Q9W4D7;
01-NOV-1995 (Rel. 32, Created)
15-SEP-2003 (Rel. 42, Last annotation
U1 small nuclear ribonucleoprotein A (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes Dev.
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Pred. No. 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stapleton M., Carlson J.W
George R.A., Guarin H., R
Rubin G.M., Celniker S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0003449; snf. GO; GO:0030532; C:small nuclear ribonucleoprotein complex; GO; GO:0007539; P:primary sex determination, soma; NAS. InterPro; IPR000504; RNA_rec_mot. Pfam; PF00076; rrm; 2.
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PROSITE; PS00030; RRM_RNP_1; 1.
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nome Biol. 3: RESEARCH0080.1-RESEARCH0080.8(2002).

FUNCTION: BINDS STEM LOOP II OF U1 SNRNA. IT IS THE FIRST SN-RNP
TO INTERACT WITH PRE-MRNA. THIS INTERACTION IS REQUIRED FOR THE
SUBSEQUENT BINDING OF U2 SN-RNP AND THE U4/U6/U5 TRI-SN-RNP (BY
SINELARITY). PLAYS A ROLE IN REGULATING SEX-LETHAL SPLICING.
SUBUNIT: BELONGS TO THE SPLICEOSOME WHERE IT IS ASSOCIATED WITH
SN-RNP U1.
                                                                                                                                                                                                                                                                                                                                             Local
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BL; L29521; AAA28903.1; -..
BL; AE003433; AAF46017.1; -..
BL; AY061491; AAL29039.1; -..
R; A54279; A54279.
SP; P09012; 3UTR.
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SIMILARITY:
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Contains 2 RNA recognition motif (RRM)
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Halley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Halley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Clays S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Cleys S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Cleys S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Collson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Collson A., G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Crafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Johnson D.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Hawas J., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Halley J.L., Martin S.L., McConnachie L., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Febra H.K., Shownkeen R., Sims S.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Habets W.J., Sillekens P.T.G., Hoet M.H., Schalken J.A., Roebroek A.J.M., Leunissen J.A.M., de Ven W.J.M., van Venrooij W "Analysis of a cDNA clone expressing a human autoimmune antigen: full-length sequence of the U2 small nuclear RNA-associated B' antigen.";
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature [3]
                                                                                                                                                                                                                                         MEDLINE-98379985; PubMed-9716128; Price S.R., Evans P.R., Nagai K.; "Crystal structure of the spliceosomal U2B'-U2A' bound to a fragment of U2 small nuclear RNA."; Nature 394.645-650(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION IN SPLICEOSOMAL COMMEDLINE=22079017; PubMed=12084575; Chung S., Zhou Z., Huddleston K.A.
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  This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
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                                                        Composed of SNRPB2, HPRP8BP and CRNKLI.
DISBASE: Patients with systemic lupus erythematosus antibodies which interact with sn RNP proteins.
SIMILARITY: BELONGS TO THE UI A/B" FAMILY.
SIMILARITY: Contains 2 RNA recognition motif (RRM)
                                                                                                                                                           FUNCTION: Involved in pre-mRNA splicing. T associated with sn-RNP U2. It binds stem lin presence of the A' protein.
SUBUNIT: Present in a spliceosome complex
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414:865-871(2001).
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  ght. It is produced through a collaboration
Bioinformatics and the EMBL outstation -
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Ol-APR-1988 (Rel. 07, Created)
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Pathogenesis-related protein R minor form precursor (PR-R) (PROB12)
(Thaumatin-11ke protein E2).
Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;
                 SEQUENCE FROM N.A.

MEDILINE-86230894; PubMed-3713832;

Cornelissen B.J.C., Hooft van Huijsduijn
"A tobacco mosaic virus-induced tobacco

Sweet-tasting protein thaumatin.";

Nature 321:531-532(1986).
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PROSITE; PS0030; RRM_RNP_1; 1.

RIbonucleoprotein; Repeat; Systemic lupus erythematosus; 3D-sr
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STRAIN-3603 V/R / Serotype V;

MEDLINE-3222988; PubMed-12200547;

Tettlelin H., Masignani V., Cleslewicz M.J., Elsen J.A., Peterson S., Tettlelin H., Masignani V., Cleslewicz M.J., Elsen J.A., Peterson S., Messels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., Madopy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Radune D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G., Fraser C.M.;
                                                                                   "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).

EMBL; AE014266; AAN00510.1; -.

TIGR; SAG1546; -.

Hypothetical protein; Complete proteome.

SEQUENCE 32 AA; 3831 MW; 2020BF60F8B8D8AD CRC64;
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Q9KQ98;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / Serotype 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vanathevan J., Bass S., Qin H., Dragoi I., Seller:

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White Balzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J
                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000).
EMBL; AE004284; AAF95248.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                            cholerae.
                                                                                                                                                                                                                                                                                    Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                TIGR; VC2102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salzberg S.I
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8F552;
Q8F552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "DNA sequence of both chromosomes
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VC2102.
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01-MAR-2003 (TrEMBLrel.
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NCBI_TaxID=173;
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45 AA; 5437 MW; FE258F385A7CA5FD CRC64;
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                                                                                                                                                          Conservative
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Last annotation update)
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Pred. No.
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hes 0;
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C STRAIN=ATCC 35092 DSM 1617 / P2;

X MEDLINE=21332296; PubMed=11427726;

X She Q. Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

A A Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Corris B.A.,

A De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.

A Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

A Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          097WA5 PRESENTED 1 18 01-OCT-2001 (TrEMBLrel. 18 01-OCT-2001 (TrEMBLrel. 18 O1-OCT-2001 (TrEMBLrel. 16 OT-CT-2001 (TrEMBLrel. 16 OT-CT-2001 (TrEMBLrel. 16 OT-CT-2001 (TrEMBLRE) 16 ORF in transposon I
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Best Local :
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                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sulfolobus solfataricus
Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2287;
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STRAIN=1330 / Biovar 1;
MEDLINE=22247741; pubMed=12271122;
Paulsen I.T., Seshadri R., Nelson K.E.,
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Brucellaceae;
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NCBI_TaxID=29461;
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                                                    proteome.
50 AA;
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6 AA; 5493 MW; FF948C9926A0DF65 CRC64;
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18, Last annotation update
ISC1058.
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Last sequence update)
Last annotation updat
                                                          0EDF90C4DFD27185 CRC64;
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Pred.
     Score
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  26;
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     DB
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Length
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                                                                                                                                                                solfataricus P2.";
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     50;
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RESULT OPERATOR OF THE PROPERTY OF THE PROPERT
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Matches
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Best Local S
Matches
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Best Local Similarity
Matches 4; Conserv
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Q48577;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ol-JUN-2001 (TrEMBLrel. 16, Created)
01-JUN-2002 (TrEMBLrel. 16, Last sequence update)
Winged helix protein CWH-6 (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa: Choc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=96118697; PubMed=7496528;

Bourseux-Eude C., Saint Girons I., Zuerner R.;

Bourseux-Eude C., Saint Girons Leptospira interrogans.";

"IS1500, an IS3-like element from Leptospira interrogans.";

Microbiology 141:2165-2173(1995).

EMBL; U13013; AAA88920.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leptospira interrogans.
Bacteria; Spirochaetes;
NCBI_TaxID=173;
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                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                               Freyaldenhoven B.S., Freyaldenhoven M.P., Iac Oncogenic potential of chicken winged helix Submitted (SEP-195) to the EMBL/GenBank/DDBJ EMBL; 037277; AAF97843.1; -. HSSP; Q63245; 2HFH,
                                                                                                                                                                                                                       Pfam; PF00250; Fork_head; 1.
ProDom; PD000425; TF_Fork_head; 1.
SMART; SM00339; FH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus.
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                                                                                                                                                                         PROSITE; PS00658; FORK_HEAD_2; PROSITE; PS50039; FORK_HEAD_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                            InterPro; IPR001766; TF_Fork_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25
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4; Conserv
                Similarity 100
4; Conservative
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AA;
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7351 MW;
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Last sequence update)
Last annotation update)
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Pred. No.
                                                                                                              B20EDB371F3AD507 CRC64
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                                        Score 26; DB 13; Pred. No. 2.1e+02;
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                     Mismatches
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helix proteins.";
nk/DDBJ databases.
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                     Indels
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Best Local :
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01-JUN-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gw. Dougherty B., Tomb J.-F., Pleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hansov van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Wedmann J., Utterback T., Watthey L., McDonald L., Artlach P., Bowmann C., Garland S., Fujli C., Cotton M.D., Horst K., Roberts K., Hatch Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Spirochaetes;
NCBI_TaxID=139;
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                                                                                                                                                           Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome annotation.";
                                                                                                                                                                                                                                                                                                                       QBLBZ1;
QBLBZ1;
Q1-QCT-2002 (TrEMBLrel. 22, Created)
Q1-QCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-QCT-2002 (TrEMBLrel. 22, Last annotation update)
Q1-QCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidieurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC
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                                           SEQUENCE FROM N.A. Brover V., Troukha Feldmann K.;
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EMBL; AE000787; AAC66097.1;
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  "Full-Length cDNA from F
Submitted (MAR-2002) to
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Plasmid; Complete proteome.
SEQUENCE 68 AA; 7927 MW; 03E39BD66E24C09A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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                                                                                                                                          Biol.
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                                                                       Troukhan M., Alexandrov N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35210
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    Arabidopsis thaliana.";
o the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spirochaetales; Spirochaetaceae;
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Last annotation updat
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Pred. No. 2.3
); Mismatches
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                                                                            Y.-P.,
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Length

68

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Rosidae;

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Borrelia.

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Best Local 9
                                                                                                                     O9VFX9
O9VFX9;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
CG11686 OR ECDNA: RH19248.
CG11686 OR ECDNA: RH19248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8WXT4;
Q1-MAR-2002 (TrEMBLrel. 20, 0
Q1-MAR-2002 (TrEMBLrel. 20, 1
Q1-QCT-2002 (TrEMBLrel. 22, 1
Winged helix transcription fi
 George
Sutton
   MEDIAME-20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.
                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Beoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                   SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF343007; AAL73344.1;
InterPro; IPR001766; TF_Fork_head.
Pfam; PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
PTODOm; PD000425; TF_Fork_head; 1.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY086916; AAM64480.1;
Hypothetical protein.
SEQUENCE 69 AA; 7446 MW;
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  R.A.,
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7446 MW;
  Wortman
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d factor-delta mRNA.",
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Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                    96487388A0DD80B2 CRC64;
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Pred. No.
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M.D.,
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Zhang
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Chen L.X.,
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        S.N.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Devilsta C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA McIndle B.E., Kodira C.D., Kraft C., McIeod M.P., McPherson D.,
RA McIndlov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang S.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A.,
RA Zheng X.H., Zhong F. N., Zhong M., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F. N., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F. N., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F. N., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F. N., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong M., Zhou S., Zhu X., Zhu X., Smith H.O.,
RA Zheng X.H., Z
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01-NOV-1996
01-NOV-1996
01-JUN-1998
                                                                                                                                               ORF72
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STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Liao G.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
George R., Gonzalez M., Guarin H., Kronmiller B., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Miranda A., Mungall C.J., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                              Plasmid pRN1.
Archaea; Crenarchaeota;
  SEQUENCE FROM N.A
                                         NCBI_TaxID=43080
                                                                 Sulfolobus
                                                                                                                         Sulfolobus islandicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                Thermoprotei; Sulfolobales; Sulfolobaceae;
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Last annotation update)
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Pred.
                                                                                                                                                                                                                                                   PRT;
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No.
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Nelson C.R., Miklos G.L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RESULT
Q9LQ57
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Best Local
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      Q9LQ57
Q9LQ57;
Q1-QCT-2000
Q1-QCT-2000
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021411;
01-NOV-1996 (TIEMBLITEL 01, Cr.
01-NOV-1996 (TIEMBLITEL 01, La.
01-MAR-2003 (TIEMBLITEL 23, La.
Hypothetical 8.3 kDa protein.
K10B3.1.
                                                                                                                                                                                                                                                                                                                                                          STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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STRAIN-Bristol N2;
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota: Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                             Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. investigating biology. The C. eleganscience 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                      "The sequence of C. elegans
Submitted (FEB-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sattung S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid pRN1.";
Plasmid 35:141-144(1996).
EMBL; U36383; AAC44108.1;
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Keeling P.J., Klenk H.P., Singh R.K., Feeley O.,
Zillig W., Doolittle W.F., Sensen C.W.;
"Complete nucleotide sequence of the Sulfolobus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96271189;
Keeling P.J., Kler
Zillig W., Doolitt
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    (TrEMBLrel. 15, (TrEMBLrel. 15,
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                                                   PRELIMINARY;
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                                                                                                                                                                                                     Score 26;
Pred. No.
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2.5e+02;
les 0;
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RESULT
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A Conn L., Conway A., Gonzalez A., Hansen N., Howing B.,
A Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsi
A Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Son
A Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Fl
A Theologis A., Ecker J.;
C Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
R EMBL, AC09317; AAF79751.1; -
R EMBL, AC09317; AAF79751.1; -
R FROSITE; PS00133; CARBOXYPEPT_ZN_2; 1
SEQUENCE 76 AA; 8899 MW; FD0CD669597E90B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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                                                                 STRAIN-SENV-D;
Tanaka Y., Pfeiffer R., Yeo A.E., Mizokami M., Edlin B.R.,
O'Brien T.R., Alter H.J., Shih J.W.;
"PCR-probe capture hybridization assay and statistical mixture
modeling for SEN virus prevalence estimation ";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB075270; BAB97340.1;
InterProc. IPR004219; TTvirus_Unk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8JX72;
01-OCT-2002
01-OCT-2002
01-MAR-2003
Pfam; PF02956; TT_ORF1;
NON_TER 1 1
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[1]
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Chao O., Brooks S., Buehler E., Dunn P., Khan S., Kim Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., I Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu Federspiel N.A., Theologis A., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-1999)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Bei B., Chin C.,
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Sakano H., Schwarz-
hera M., Yu G., Davis R.,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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B., Chin C., Chiou J., Choi E.,
Hansen N., Howing B., Koo T., Lam B.,
Liu J., Liu S., Mukharsky N.,
ano H., Schwartz J., Southwick A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                ssDNA viruses
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /SIDS1/gcgdata/gen

2: /SIDS1/gcgdata/gen

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48
1 NGWYPW 6
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Match
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Gapop 10.0 , Gapext 0.5
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ABG03291
AAB26455
AAB20924
AAG55477
ABG59477
ABB44094
ABB26986
AAM65117
AAM77824
                                                                                                                                                                                                                                                                                                                      SUMMARIES
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                                                                                                                    Novel human diagno
Drosophila melanog
Drosophila odorant
Mandrill immunodef
                                                                                                                                                                                                                                            Description
                                                Human liver peptid
Peptide #11600 enc
Protein #8985 enco
  Human brain expres
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PRO1784  PRO1784  human see  secreted  pro poly  pro poly  secreted  pro poly  secreted  in encode  dopsis th  dopsis th  dopsis th  dopsis th  dopsis th  formally a  dopsis th  formally a  formally	Peptide #8160 enco Peptide #12079 enc Human peptide enco Arabidopsis thalia Propionibacterium N. gonorrhoeae ami Human PRO 1784 (UNO Human Colon cancer Protein of the inv

## ALIGNMENTS

RESULT 1 ABG03291

ABG03291 standard; Protein; 562 AA.

13-FEB-2002 (first entry)

Novel human diagnostic protein #3282.

ABG03291;

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PT XXX PX
                                                                                                     WPI; 2001-639362/73.
N-PSDB; AAS67478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                    Tang
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New isolated polynucleotide and encoded polypeptides, useful in

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RESULT 2
AAB26455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating CC inaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC disorders, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed constitution, but was obtained in electronic format directly from WIPO at the first invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 5
                 Disclosure;
                                             Novel nucleic acid encoding an insect odorant receptor, modulator compounds that are useful in controlling pest
                                                                                                    N-PSDB; AAA94853
                                                                                                                                                                                                                                                       25-FEB-2000; 2000WO-US04995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB26455 standard; Protein; 403
                                                                                                                     WPI; 2000-572081/53
                                                                                                                                                                                      (UYCO ) UNIV
                                                                                                                                                                                                                         25-FEB-1999;
                                                                                                                                                                                                                                                                                                                           W0200050566-A2
                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                           Odorant receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster odorant receptor DOR83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB26455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostics, forensics, responsible for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 GWYPW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GWYPW 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 5; Conserv
                                                                                                                                                      LB,
                 Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                      COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                       99US-0257706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                 86;
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                                                                                                                                                                                                                                                                                                                                                                                           fruit
              176pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.5%;
                                                                                                                                                     Ю,
                                                                                                                                                                                                                                                                                                                                                                                         fly;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene mapping, identification of mutations disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                     DOR83; odour recognition; pest control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 562;
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                                               population
                                                         for identifying
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RESULT 3
AAB20924
Sequences AAB20901-B20949 represent Drosophila melanogaster odorant CC receptors. These proteins function as olfactory receptors, and CC are thought to be members of the G protein-coupled receptor (GPCR) superfamily, which is characterised by the presence of 7 CC transmembrane helices. Nucleic acids encoding the Drosophila odorant CC receptors may be used to generate expression constructs, host cells which express CC containing such constructs, and transgenic insects. Cells which express CC which modulate expression of these genes, and in methods to identify receptor binding partners. The Drosophila odorant receptor nucleic acids come as those which damage crops or transmit disease. The odorant receptor proteins may be used to identify agents which modulate their receptor proteins may be used to identify agents which modulate their activity, to identify binding partners, as antigens to raise antibodies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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Best Local S
Matches 5
                                                                                                                                                                                                                                                              Claim 12;
                                                                                                                                                                                                                                                                                        New nucleic acid encoding a Drosophila olfactory receptor, useful for identifying modulating agents - \,
                                                                                                                                                                                                                                                                                                                                                                                                Carlson JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200043410-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the previously identified Drosophila melanogaster odorant receptor DOR83. The odorant genes and proteins, such as those provided by the invention, are useful as they aid in the study of the olfactory organ in mammals, as well as aiding the understanding of the link between odour recognition and behaviour in insects. They also enable the identification of compounds capable of activating and inhibiting the receptors, allow the control of pest populations via the use of alarm odour ligands and via the use of ligands which interfere with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2000; 2000WO-US01823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Odorant receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila odorant receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insect behaviour modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interaction between odorant ligands and receptors associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein-coupled
                                                                                                                                                                                                                                                                                                                                                                2000-543246/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 NTWYPW 181
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5; Conserv
                                                                                                                                                                                                                                                           Page 184-185; 303pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   odour detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       403
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                                                                                                                                                                                                                                                                                                                                                                                                Kim J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0117132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; olfactory receptor;
                                                                                                                                                                                                                                                                                                                                                                                                Clyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPCR superfamily; transgenic insect;
on; pest control; pollinator attraction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    odour
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                Warr
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simian immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simian immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG65229 standard; Protein; 853
                                                                                                       Sequence
                                                                                                                              The present invention relates to a new mandrill immunodeficiency virus SIM27, which can be used to detect antibodies directed against the virus. The present sequence is the ENV protein described in the exemplification of the invention.
                                                                                                                                                                                               Example 3; Page 27; 47pp; Norwegian.
                                                                                                                                                                                                                         New mandrill immunodeficiency virus SIM27 useful for antibodies directed against the virus - \,
                                                                                                                                                                                                                                                                WPI; 2001-201061/20.
                                                                                                                                                                                                                                                                                         Guertler LG,
                                                                                                                                                                                                                                                                                                                   (DADE-) DADE
                                                                                                                                                                                                                                                                                                                                             03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                05-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                          NO200003889-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mandrill immunodeficiency virus SIM27 ENV protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG65229;
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 416 NVWYPW 421
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5; Conserv
                                                  . Similarity
5; Conserv
                        NGWYPW 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   414 AA;
                                                                                                       853
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                                                    Conservative
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83.3%;
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Pred. No. 1.3e+02;
                                                    Score 39; DB
Pred. No. 3.9e
0; Mismatches
                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV;
                                                                                                                                                                                                                                                                                           Deloko
                                                     DB 22; I
3.9e+02;
hes 1;
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                                                                                                                                                                                                                                                                                          YBD,
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                                                                             Length 853;
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RESULT 5
ABG5971
ID ABG57
XX ABG597
XX ABG597
XX ABG59 XX
XX Huma
XX Huma
XX Huma
XX Hope
XX The
XX
RESULT 6
ABB44094
ID ABB4
XX
AC ABB4
XX
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Best Local S
Matches 4
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-063256.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG59477 standard; Peptide; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488898/53.
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                                                                                     ABB44094 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Pred. No.
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ABB44094;

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RESULT 7
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Matches 4
                                                             Human; gene expression; heardiovascular disease; he congenital heart disease.
  09-AUG-2001
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                      WO200157274-A2
                                          Homo sapiens.
                                                                                                         Protein #8985
                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
                                                                                                                              23-JAN-2002
                                                                                                                                                   ABB26986;
                                                                                                                                                                      ABB26986 standard;
                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG,
                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the ed specification, but was obtained in electronic format directly WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome-derived single exon nucleic acid probes useful
zing gene expression in human fetal liver -
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                                                                                                                                                                                                                                               1 NGWYPW 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 36729; 639pp + sequence listing; English
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                                                                                                                                                                                                                                                                                                              39
                                                                                                                                                                                                                                                                    Conservative
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-02346359.
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                            ΑĄ;
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                                                                                                     encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded
                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                              79.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression; single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                                                        hypertension;
                                                                                  heart; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by human
                                                                                                                                                                      39
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                                                                                                                                                                                                                                                                           Score 38;
Pred. No.
                                                                                                    for measuring heart cell gene
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                                                                        cardiac
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25;
                                                                                  vascular system;
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RESULT 8
AAM65117
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Best Local
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 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                      09-AUG-2001
                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                              Human brain expressed single exon probe encoded protein SEQ ID NO: 37222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the publicular ished not sequence.
                                                                             30-JAN-2001;
                                                                                                                              WO200157275-A2
                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                epilepsy; cancer
                                                                                                                                                                                                                                                             05-NOV-2001
                                                                                                                                                                                                                                                                                     AAM65117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                          SGWHPW 15
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2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-02346359.
; 2000US-0236359.
                                                                             2001WO-US00667
                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                              Protein;
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66.78;
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Pred. No. 25;
2; Mismatches
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25;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human probes which are derived from genomic sequences expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-)
                                                                                                                                                                   Penn
                                                                                                                                                                                                                                                                            21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM77824 standard; Protein;
                                                                                                                                                                                                           (MOLE-)
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                                                     genome-derived single exon nucleic acid probes zing gene expression in human bone marrow -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGWYPW 6
                                                                                                                                                                                                           MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                   Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO: 37222; 650pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39
                                                                                                                                                                                                                                                                        2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     marrow expressed exon; gene expression analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0236359
2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US00668
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                 ID NO:
                                                                                                                                                                   몼
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed probe encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia; lymphoma; myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.2%;
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                                                                                                                                                                   Chen W,
                 38130; 658pp + Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes
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Pred.
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                                                                                                                                                                     Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for analyzing gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                 Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID
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                                                                                useful
                    English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probe;
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RESULT 10
AAM21726
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                        The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encode by one such probe. The SENPs are derived from human HeLa cells. The SENE can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefor useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; human; microarray; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #8160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM21726
                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157278-A2
Sequence
                                                                cervical cancer
                                                                                                                                                                                   Claim 27; SEQ ID No 26552; 487pp;
                                                                                                                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                   2001-488901/53.
                                                                                                                                                                                                                                                                            SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                            Hanzel
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 39
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; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
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Pred.
                                                                                                                                                                                                                                                                             Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
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25;
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                                                                                           from human cervical probes are therefore
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Query Match

79.2%;

Score

38;

DB 22;

Length

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RESULT 12
ABG46855
ID ABG46
XX
AC ABG46
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DT 19-AU
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                                                                                                                                                                           RESULT 11
AAM38042
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                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
      19-AUG-2002
                                             ABG46855 standard;
                                                                                                                                                                                                                                                               Claim 27; SEQ ID No 38311; 654pp;
                                                                                                                                                                                                                                                                                  analyzing
                         ABG46855;
                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; microarray; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #12079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM38042;
                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                   SG,
                                                                                                                                                                                              genetic disorders.
                                                                                              10 SGWHPW 15
                                                                                                                 1 NGWYPW 6
                                                                                                                                   l Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 SGWHPW 15
                                                                                                                                                                                                                                                                                                                                                                                    2000;
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                                                                                                                                                                                                                                                                                  gene expression
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                                                                                                                                    Conservative
     (first entry)
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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2000US-0207456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-US00663
                                                                                                                                                                           A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded
                                            Peptide; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; placenta;
                                                                                                                                             79.2%;
66.7%;
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                                                                                                                                                                                                                                                                                  in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probe for
                                                                                                                                  Score 38; DB Pred. No. 25; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39
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;:
                                                                                                                                                                                                                                                                                  human placenta
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                                                                                                                                                                                                                                                                                                                                   Rank
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                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                  DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         measuring placental gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                       22;
                                                                                                                                   0;
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                                                                                                                                                      Length 39;
                                                                                                                                   Indels
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Human; single exon probe; asthma; lung
                                 Human
                               peptide
                              encoded by genome-derived single
                               exon
                              probe
                              SEQ ID 36520
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chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease. cancer; COPD; ILD; interstitial lung disease;

Homo sapiens.

WO200186003-A2

15-NOV-2001

30-JAN-2001; 2001WO-US00665

21-SEP-2000; 27-SEP-2000; 03-AUG-2000; 26-MAY-2000; 30-JUN-2000; 04-FEB-2000; 2000US-180312P. 2000US-207456P. 2000US-0608408. 2000US-0632366. 2000US-234687P. 2000US-236359P. 2000US-236359P. 2000US-0024263.

(MOLE-) MOLECULAR DYNAMICS INC

Penn Hanzel DK, Chen W, Rank DR;

WPI; 2002-114183/15

measure gene expression in human lung samples Spatially-addressable set of single exon nucleic acid probes, used ç

Claim 27; ij ö 634pp; English.

CC nucleic acid expressed in the human lung; measuring gene expression in a CC sample derived from human lung, comprising (a) contacting the array with CC a collection of detectably labeled nucleic acids derived from human lung (masuring the label detectably bound to each probe of CC (a) algorithmically predicting at least one exon from genomic sequences (C (a) algorithmically predicting at least one exon from genomic sequences (c) the eukaryote; and (b) detecting specific hybridisation of detectably CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, of having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, CC comprising (a) identifying exons from genomic sequence by the method CC above and (b) measuring the expression of each of the exons in several CC tissues and/or cell types using hybridisation to a single exon CC expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the expression analysis, and for identifying exons in a gene, particularly CC using human lung derived mRNA and for the study of lung diseases (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary CC thorsis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, nulmonary and content of the content of the study of the pulmonary of the study of the secondary. The probes are used for gene approached the secondary of the study of lung disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary content of the secondary of the seco probes; Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, nucleic acid probes for measuring gene expression in a sample derive from human lung comprising single exon nucleic acid probes having or 12614 nucleic acid sequences mentioned in the specification, or the complements or the 12387 open reading frames derived from the 12614 The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derive Also included are a microarray comprising the novel set of the novel set of probes which hybridise at high stringency to a derived their one of

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RESULT 13
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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1; Mismatches
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                    Gaps
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RESULT 15
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ID AAU477
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                                                                            Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a CC sample with a binding agent that binds to the proteins of the invention CC and determining the amount of bound protein in the sample. The CC polypeptides may be used as antigens in the production of antibodies convergulate expression and activity of P. acnes production of antibodies CC diagnostic agents for determining P. acnes propagated as a construction of the refore treat P. acnes infections. The antibodies may also be used as CC diagnostic agents for determining P. acnes presence, for example, by CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO at the first manning the printed of the printed contraction of the printed contraction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW, Persing DH, N
L'maisonneuve J, Zhang Y,
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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1: /cgn2_6/ptodata/1,

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US-08-915-314-34
US-08-915-316-7
US-08-925-316-7
US-08-828-323-10
US-09-194-52A-1132
US-09-194-52A-1132
US-09-194-905-118
US-09-194-905-118
US-09-252-991A-27442
US-08-860-255A-4
US-08-860-255A-4
US-08-118-7
US-08-30-476-118
US-08-30-476-118
US-08-311-784A-30
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20, Ap	S Appl	5, Appli	5, Appl	19257,	20649,	3, Appl	25248,	26691,	2, Appl	15, Appl	21, Appl	19648,	1, Appli	1, Appli	5731, A	26087,	211, App

## ALIGNMENTS

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Patent No. 656513

GENERAL INFORMATION:
APPLICANT: GENERILER, Lutz Gerhard
APPLICANT: HAUSER, Hans Peter
APPLICANT: HAUSER, Hans Peter
APPLICANT: LEXERNG, Leopold
APPLICANT: KAPTUE, Leopold
APPLICANT: KAPTUE, LAZAR
TITLE OF INVENTION: LENTIVYRUS FROM THE GROUP OF
TITLE OF INVENTION: (MANDRILLUS LEUCOPHAEUS) AND
FILE REFERENCE: 067595/0106
CURRENT APPLICATION NUMBER: US/09/625,972
CURRENT FILING DATE: 2000-07-29
PRIOR APPLICATION NUMBER: DE 199 36 003.0
PRIOR FILING DATE: 1999-08-03
                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-09-625-972-25
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQ
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 16759
LENGTH: 115
TYPE: PRT
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Best Local
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
NUMBER OF SEQ ID NOS:
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US-09-252-991A-28172
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US-09-625-972-25
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GENERAL INFORMATION:
                              Query Match
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LENGTH: 555
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LENGTH: 236
TYPE: PRT
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APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Patent No. 6551795
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Best Local Similarity
                                                                                                                                                                                                                                    PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                       FEATURE:
                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
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MITTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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                            DB 4;
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                                                                                                                                                                                                                                                                                                                                                           AND THERAPEUTICS
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                                                                             are unknown.
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                                                                                                  GENERAL INFORMATION:
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                            APPLICANT:
                                                        APPLICANT:
                                                                     APPLICANT:
                                                                                   APPLICANT:
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               APPLICANT:
                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 682-603
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Erfle, Do
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: NO. 6180604tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                  TYPE:
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STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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    INVENTION:
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                                                                                                                                                                                                                                                                                                                                                  amino acid
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Fraser, Janet R.
West, Michael H.P.
McNicol, Patricia J.
PENTION: COMPOSITIONS
                                                      Taylor, Robert
Erfle, Douglas
                                                                                                                            Application US/09030619B
                                                                                  Krieger, Timothy J
                                                                                                                                                                                                                                                                                                                                                               13 amino acids
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                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-1997
N: 42'
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                                                                                                                                                                                                                                                                 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOSITIONS AND METHODS FOR TREATING INFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
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Pred. No
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 AND METHODS FOR TREATING
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ches 0;
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SOFTWARE: FastSEQ for Windows Version 5.0 SEQ ID NO 35 LENGTH: 13 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Indolicidin Analogue US-09-030-619-35
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Best Local Similarity 100.
4; Conservative
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Query Match
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TITLE OF INVENTION:
FILE REFERENCE: 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
CUMBER OF SEQ ID NOS: 232
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: NO. 6538106tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: (206) 682-631
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iquence 34, Application US/09667486
itent No. 6538106
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED an
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                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/667,486
FILING DATE: 22-Sep-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/915,314 FILING DATE: 20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Washington
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                                                                            TOPOLOGY: 11n
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                                                                                                                             LENGTH:
                                                        DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taylor, Robett Erfle, Douglas AND METHODS FOR TREATING AVENTION: COMPOSITIONS USING ANALOGUES OF INDOLICIDIN
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                                                                                                                                 13 amino acids
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100.0%; Pred. No.
Live 0; Mismatc
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                                                                                            <Unknown>
Score 36;
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5.7;
DB 4; Length 13;
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US-09-355-166-7
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SEQ ID NO 7
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Patent No. 6316241
GENERAL INFORMATION:
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Matches 4; Conserv
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Best Local 9
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CURRENT FILING DATE: 1999-07-20
                                                                     TELEFAX: (203)268-1951 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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TYPE: PRT
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                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
                                                                                                                                                                                                                               SOFTWARE: Microsoft Word 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                         SEQUENCE CHARACTERISTICS LENGTH: 334 amino acid
                                                                                             REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
  OLECULE TYPE:
                                                                                                                                           NAME: George M. Yahwak REGISTRATION NUMBER: 2
                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: Microso
                                                                                                                                                                                                                                                                          COMPUTER:
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              ropology:
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o. 566800
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                             amino acid
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25 Skytop Drive
                                            334 amino acids
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                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Michael E. O'Donnell
VENTION: DNA POLYMERASE III
                                                                                  (203)268-1951
                                                                                                                                                                                                                                                                        Macintosh
                linear
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peptide
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                                                                                                                                           26,824
                                                                                                                               CRF D-1056CIP
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Pred. No.
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RESULT 12
US-09-134-078-62
US-09-134-078-62
; Sequence 62, Application US/09134078
; Patent No. 636844
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE I
                                                                                                                                               밁
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US-09-198-452A-1132
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                                                                                                                                                                                                                                                                        ; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1132
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US-08-828-323-10
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US-08-828-323-10
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                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Griffals, R.
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, frag
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis,
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DNA POLYMERASE III HOLOENZYME FILE REFERENCE: 19603/10214

CURRENT APPLICATION NUMBER: US/08/828,323A

CURRENT FILING DATE: 1997-03-28

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SEQ ID NO 1132
LENGTH: 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1132, Application US/09198452A
Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: O'Donnell, Michael
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24
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                                                                                                                                                                                                                            Local
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                                                                                                                                             28 WYPW 31
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100.0%; Pr
 Edward J.
GLYCOSIDASE ENZYMES
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100.0%; Pred. No.
tive 0; Mismatcl
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Pred. No.
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Pred. No.
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3.2e+02;
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1.6e+
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; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-27442
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US-09-252-991A-27442
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; FRAGMENT TYPE:
US-09-134-078-62
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                              SEQ ID NO 27442
LENGTH: 705
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27442, Application US/09252991A Patent No. 6551795
                 Query Match
Best Local Similarity
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                   PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
RAPPLICATION UNMBER: 08/949,026
FILING DATE: 10-CCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/024002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 858/677-1465
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CITY: San Diego
STATE: CA
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4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             684 amino acids
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 Conservative
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66.7%;
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               Score 36; DB 4;
Pred. No. 3.3e+02;
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Pred. No.
 Mismatches
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                                 Length 705;
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1 NGWYPW 6 | |:|| 534 NTWFPW 539

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SOPTWARE: FastSEQ for W1 SEQ ID NO 4
LENGTH: 212
TYPE: PRT
ORGANISM: homo sapiens
US-08-860-255A-4
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US-08-484-905-118
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                                                                                                                                                                    Sequence 118, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
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Best Local :
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CURRENT FILING DATE: 1997-06-26
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PRIOR FILING DATE: 1995-10-30
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                      APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods
TITLE OF INVENTION: Determinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OR APPLICATION NUMBER: 60/00
OR FILING DATE: 1995-11-22
OR APPLICATION NUMBER: 60/00
OR FILING DATE: 1995-12-31
OR APPLICATION NUMBER: 60/01
OR FILING DATE: 1996-03-20
OR APPLICATION NUMBER: 60/01
OR FILING DATE: 1996-03-20
OR APPLICATION NUMBER: 60/01
OR FILING DATE: 1996-03-20
OR APPLICATION NUMBER: 60/01
OR FILING DATE: 1996-05-17
OR APPLICATION NUMBER: 60/01
OR FILING DATE: 1996-05-17
OR APPLICATION NUMBER: 60/02
OR FILING DATE: 1996-05-17
OR FILING DATE: 1996-06-13
OR FILING DATE: 1996-06-13
OR APPLICATION NUMBER: 60/02
OR APPLICATION NUMBER: 60/02
OR FILING DATE: 1996-06-13
OR APPLICATION NUMBER: 60/02
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64 NGGYPW 69
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ADDRESS:
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1996-08-07
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1996-05-17
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Pred. No. 1.4e+02;
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Query Match
Best Local Similarity
Tatches 4; Conserve
Search completed: August 20, 2003, 12:44:22 Job time : 5.15663 secs
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                                                                                                                                                                                                            US-08-484-905-118
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                              TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/792,473
                                                                                                                                                                                                                     LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS-MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 15-NOV-1991 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                    1 NGWYPW 6
                                                                   3 SGWVPW 8
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1300 I Street, N.W., Suite 700
                                                                                                                                      Conservative
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Pred. No. 1
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                                                                                                                                                     DB 2;
1.8e+02;
                                                                                                                                                                    Length 273;
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                                                                                                                                   Gaps
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd

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Perfect score:
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1: /cgn2_6/ptodata/I/pubpaa/Pi
2: /cgn2_6/ptodata/I/pubpaa/Pi
3: /cgn2_6/ptodata/I/pubpaa/Pi
4: /cgn2_6/ptodata/I/pubpaa/Pi
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6: /cgn2_6/ptodata/I/pubpaa/Pi
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9: /cgn2_6/ptodata/I/pubpaa/U
9: /cgn2_6/ptodata/I/pubpaa/U
10: /cgn2_6/ptodata/I/pubpaa/I
11: /cgn2_6/ptodata/I/pubpaa/I
12: /cgn2_6/ptodata/I/pubpaa/I
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length: 2000000000
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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// Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
// Cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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1 US-09-946-374-390
12 US-10-015-387A-390
12 US-10-006-130A-390
12 US-10-199-672-376
12 US-10-199-672-376
12 US-10-194-457-376
14 US-10-194-457-376
15 US-10-174-596-376
16 US-10-174-596-376
17 US-10-174-598-376
18 US-10-174-5737-376
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US-10-156-761-7581
US-10-183-708-92
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Sequence 32, Appl
Sequence 92, Appl
Sequence 42284, A
Sequence 390, App
Sequence 390, App
Sequence 390, App
Sequence 376, App
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29 ,	28	27	26	25	24	23	22	21	20	19	18	17	16	
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-10-174-576-37	US-10-173-705-376	-10-173-697-37	-10-173-695-37	-10-176-991-37	-10-184-658-37	-10-176-993-37	-10-176-992-37	-10-176-987-37	-10-176-985-37	-10-176-750-37	-10-176-747-37	-10-176-492-37	-10-176-488-37	-10-175-743-37	-10-175-740-37	-10-175-739-37	-10-174-588-37	-10-174-582-37	-10-174-579-37	-174-572-37	-10-173-700-37	-10-180-557-37	-10-180-552-37	-10-176-913-37	-10-176-757-37	-10-176-482-37	-10-175-752-37	-175-738-37	-10-173-706-37	
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## ALIGNMENTS

RESULT 1 US-09-300-425B-32

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; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B; OTHER INFORMATION: antibody clone US-09-300-425B-32
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SEQ ID NO 32
LENGTH: 6
TYPE: PRT
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GENERAL INFORMATION.

APPLICANT: VARI, LOTEBIZO

APPLICANT: VITI, Francesca

APPLICANT: BIRCHLER, Manfred

TITLE OF INVENTION: SECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES

TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF

TITLE OF INVENTION: ANGIGENESIS

FILE REFERENCE: SCH-1733P1

CURRENT APPLICATION NUMBER: US/09/300,425B

CURRENT FILING DATE: 1999-04-28

CURRENT FILING DATE: 1999-04-38

CURRENT APPLICATION NUMBER: 09/075,338
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                                                                                  Matches
                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                    Local
                                     1 NGWYPW 6
                                                                              6; Conserv
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                                                                                Conservative
                                                                                                  100.0%; Score 48; DB 11; 100.0%; Pred. No. 4.4e+05;
                                                                                  0,
                                                                                Mismatches
                                                                                                                        Length 6;
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RESULT

-10-156-761-7581

, Application US/10156761

US20030119018A1

INFORMATION:

OMURA, SATOSHI IKEDA, HARUO

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RESULT 4
US-09-864-761-42284
; Sequence 42284, Application US/09864761
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Best Local :
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Best Local
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 09/932,227
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: PCT/US00/04995
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 09/257,706
PRIOR FILING DATE: 1999-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GENES ENCODING INSECT ODORANT RECEPTORS AND USES THEREOF FILE REFERENCE: 0575/58715-AA-PCT-US/JPW/ADM/BJA
CURRENT APPLICATION NUMBER: US/10/183,708
CURRENT FILING DATE: 2002-06-25
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                     LENGTH: 403
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ENGTH: 318
                                                                                           176 NTWYPW 181
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HORIKAWA, HIROSHI
                                                                                                                                                               Conservative
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83.3%;
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83.3%;
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Pred. No.
                                                                                                                                                                               Score 40;
Pred. No.
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53;
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US-09-864-761-42284
                     Query Match
Best Local
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CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION DATE: 2000-02-04
PRIOR APPLICATION DATE: 2000-02-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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                                                                                                                                                                  OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.0THER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1 OTHER INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 0.0THER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.0THER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
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FILING DATE: 2001-01-29
R OF SEQ ID NOS: 49117
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  Similarity 4; Conserv
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Hanzel, David K.
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79.2%; ilarity 66.7%; Conservative
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WMBER: US 09/608,408
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CURRENT FILING DATE: 2001-09-04
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OR FILING DATE: 1998-09-01
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Williams, P. Mickey
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Hillan, Kenneth J.
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Margaret Ann
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DR FILING DATE: 1998-10-07

DR APPLICATION NUMBER: 60/103315

DR APPLICATION NUMBER: 60/103328

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DR FILING DATE: 1998-10-07

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FILING DATE: 1998-10-01
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APPLICATION NUMBER: 60/102570
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FILING DATE: 1998-09-29
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                                                                                                                                  48 NGWYIW 53
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                                                                                                                                                                               1 NGWYPW 6
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                                                                                                                                                                                                                                                                                                                NUMBER: 60/105807
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Pred. No. 1.4e+02;
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Mismatches

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Prior Application removed -
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 390
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-10-006-130A-390
Query Match
Best Local Similarity
---hes 5; Conserve
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Best Local S
Matches 5
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NUMBER OF SEQ ID NOS: 477
SEQ ID NO 390
LENGTH: 146
TYPE: PRT
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APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C54
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Gao, Wei-Qiang
Goddard, Audrey
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Gao, Wei-Qiang
Goddard, Audrey
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                                                                                                                                                                                                                                                      Paoni, Nicholas F.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth J.
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Desnoyers, Luc
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Pred. No.
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Pred. No.
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RESULT 8
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                                                      US-10-006-172A-390
Sequence 390, Application US/10006172A
Diblication No. US20030153000A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P
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Best Local S
Matches 5
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PRIOR EILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
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APPLICANT:
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FILING DATE: 1997-10-28
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FILING DATE: 1997-10-28
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FILING DATE: 1997-10-24
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5; Conserv
         Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan 1.
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Watanabe, Colin K.
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Ferrara,
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Pred. No. 1.4e
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1.4e+02;
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PRIOR FILING DATE: 60/0 PRIOR APPLICATION NUMBER: 60/0 PRIOR FILING DATE: 1998-09-09 PRIOR FILING DATE: 60/
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PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
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PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-09-01
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FILING DATE: 1998-09-02
APPLICATION NUMBER: 60/098821
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FILING DATE: 1998-09-02
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                                           APPLICATION NUMBER: 60/7
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                            FILING DATE: 1998-0 APPLICATION NUMBER:
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APPLICATION NUMBER: 60/:
FILING DATE: 1998-09-16
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FILING DATE: 1998-09-10
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Gao, Wei-Qiang
Goddard, Audrey
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Hillan, Kenneth J.
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Grimaldi, Christopher
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RESULT 10
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FILING DATE: 1998-10-22
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FILING DATE: 1998-10-20
APPLICATION NUMBER: 60/105104
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FILING DATE: 1998-10-14
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FILING DATE: 1998-10-08
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FILING DATE: 1998-10-07
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FILING DATE: 1998-10-07
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     INVENTION: SEC
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                               Smith, Victoria Watanabe, Colin K Wood, William I.
                                                                                               Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                               Baker, Kevin P. Chen, Jian
                                                                                   Pan, James
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o. US20030153036A1
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1.4e+02;
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OR APPLICATION NUMBER: 60/101471
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APPLICATION NUMBER: 60 FILING DATE: 1998-09-1

60/101071

FILING DATE: 1998-09-23
APPLICATION NUMBER: 60/101479
APPLICATION 1998-09-23
TTING DATE: 1998-09-27101738

APPLICATION NUMBER: 60/101477

APPLICATION NUMBER: 60/101476

1998-09-23

LING DATE:

APPLICATION NUMBER: 60/101738

1998-09-24

APPLICATION NUMBER: 60/102965 FILING DATE: 1998-10-02 APPLICATION NUMBER: 60/103258 FILING DATE: 1998-10-06

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60/103314

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APPLICATION NUMBER: 60/102240 FILING DATE: 1998-09-29 APPLICATION NUMBER: 60/102307

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APPLICATION NUMBER: 60/102207

LING DATE: 1998-09-29

OR APPLICATION NUMBER: 60/100930
OR FILLING DATE: 1998-09-17
OR APPLICATION NUMBER: 60/101014
OR FILLING DATE: 1998-09-18
OR APPLICATION NUMBER: 60/101068
OR APPLICATION NUMBER: 60/101068
OR FILING DATE: 1998-09-18

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APPLICATION NUMBER: 60/100849
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FILING DATE: 1998-09
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1998-09-1998-09-1998-09-17

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APPLICATION NUMBER: FILING DATE: 1998-09

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ACIDS ENCODING THE SAME

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US-10-187-749-376
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SEQ ID NO 376
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APPLICANT:
                           PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR EILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C296
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CURRENT FILING DATE: 2002-07-01
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CURRENT FILING DATE: 2002-07-11
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TYPE: PRT
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FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063486
FILING DATE: 1997-10-21
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Similarity 83.3%;
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Watanabe, Colin K.
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Pred. No. 1.4e+02;
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US-10-052-586-376
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PRIOR FILING DATE: 1997-10-24
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TYPE: PRT
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FILING DATE: 1997-10-28
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                                                                                                                                FILING DATE: 1997-10-28
                                                                                                                                                  APPLICATION NUMBER: 60/063544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NGWYPW 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe, Colin K. Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/10052586 o. US20020127584A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      data removed - See File Wrapper or PALM.
                                                                                                                                                                                                  1997-10-28
                                                                1997-10-29
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MBER: 60/064103
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                                                60/063870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 12;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
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R APPLICATION NUMBER: 60/06
R FILING DATE: 1997-11-13
R APPLICATION NUMBER: 60/06
R APPLICATION NUMBER: 60/06
JR FILING DATE: 1997-11-21
JR APPLICATION NUMBER: 60/01
JR FILING DATE: 1997-11-24

60/066466 60/066120 60/065311 1-13

PRIOR

R APPLICATION N R FILING DATE: R APPLICATION N R FILING DATE: R APPLICATION N

NUMBER: 60/0: 1997-12-18

R FILING DATE:
R APPLICATION N
FILING DATE:

NUMBER: 60/069870: 1997-12-17

1997-12-1997-12-11

60/069425

R FILING DATE:
R APPLICATION NI
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R APPLICATION NI
R FILING DATE:
R APPLICATION NI

NUMBER: 60/0: 1998-03-20

NUMBER: 60/077649: 1998-03-11

NUMBER: NUMBER:

60/077632 60/077450 60/068017

1998-03-10

1998-03-

NUMBER:

60/078939 60/078886

1998-03-20

R FILING DATE:
R APPLICATION NI
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NUMBER: NUMBER:

1998-03-27

1998-03-31

FILING DATE:
APPLICATION N

NUMBER: 60/079664: 1998-03-27

PRIOR

FILING DATE: 1997-1: APPLICATION NUMBER: APPLICATION

APPLICATION NUMBER: 60/066772 FILING DATE: 1997-11-24

NUMBER: 60/069335

PRIOR R APPLICATION NUMBER: 60/08 R FILING DATE: 1998-06-10 R APPLICATION NUMBER: 60/08 R FILING DATE: 1998-06-10 R FILING DATE: 1998-06-10 R FILING DATE: 1998-06-04
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R FILING DATE: 1998-06
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: 60/ FILING DATE: 1998-06-05 FILING DATE: 1998-0: APPLICATION NUMBER: APPLICATION FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/ FILING DATE: 1998-05-15 FILING DATE: 1998-06-10 APPLICATION NUMBER: FILING DATE: 1998-05-22 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION PRILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION N FILING FILING ATION NUMBER: 60/085573 DATE: 1998-05-15 ATION NUMBER: 60/085579 DATE: NUMBER: 60/0: 1998-05-15 NUMBER: NUMBER: 1998-06-10 1998-06-12 1998-06-10 TUMBER: 60/089512 1998-06-16 1998-06-10 1998-06-10 1998-05-28 1998-05-22 1998-05-18 1998-05-07 1998-05-60/088861 60/088202 60/087759 60 60/089105 60/088876 60/088863 60/088826 60/088825 60/088824 60/088811 60/088740 60/088738 60/088722 60/088655 60/088326 60/088217 60/088212 60/088167 60/088033 60/088029 60/088028 60/088025 60/087827 60/087609 60/087098 60/086486 60/086392 60/086023 60/085700 60/085582 60/085580 /087208

R FILING DATE:
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60/084643 60/084640 60/084639 60/084414 60/084366 60/083559 60/083499 60/083496 60/083495

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DATE: 1998-04-22

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60/082797

NUMBER: 60/083322

APPLICATION NUMBER: 60/0 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/0

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998-04-29

PRIOR PRIOR PRIOR PRIOR

APPLICATION N FILING DATE:

NUMBER:

60/082569

998-04-21

FILING DATE: APPLICATION

NUMBER: 60/082568: 1998-04-21

PRIOR

ATION NUMBER: 60/082704 DATE: 1998-04-22

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FILING DATE: APPLICATION N

DATE:

NUMBER: 60/0: 1998-04-15

60/081838 60/081195 60/081070 60/081049 60/080333

FILING DATE: 1998-U4 UC APPLICATION NUMBER: 60/C APPLICATION NUMBER: 60/C

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FILING DATE:
APPLICATION N

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1998-04-01

APPLICATION NUMBER: 60/ FILING DATE: 1998-03-31

60/080194 60/080107 60/079786

APPLICATION NUMBER: 60/080327

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US-10-176-758-376
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-376
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APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L.
Tames
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin I
APPLICANT: Ban, James
APPLICANT: Watanabe, Colin
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 376
                                                                                                                                                                                                              Sequence 376, Application US/10176758 Publication No. US20030008353A1
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.2%;
Best Local Similarity 83.3%;
                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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Similarity 83.3%;
5; Conservation
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                Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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                                                                                        Gurney, Austin L.
                                                                                                         Goddard, Audrey
Godowski, Paul J.
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Pred. No. 1.4e+02;
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Search completed: August 20, Job time: 7.50602 secs
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Best Local Similarity
"atches 5; Conservations
                                                                                                                                                                                                     ; ORGANISM: Homo Sapien US-10-175-737-376
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US-10-175-737-376
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                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/175,737

CURRENT FILING DATE: 2002-06-19

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 376

LENCTH: 146

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul :
APPLICANT: Gurney, Austin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 376
LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 376, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/176,758 CURRENT FILING DATE: 2002-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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TYPE: PRT
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                                                                   48 NGWYIW 53
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                             Zhang,Zemin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/10175737 o. US20030013153A1
                                                                                                                                    Conservative
                                                                                                                                                  79.28;
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83.3%;
               2003, 13:16:47
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Pred. No. 1.4e+02;
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Pred. No. 1.4e+02;
0; Mismatches 1
                                                                                                                                  Mismatches
                                                                                                                                                                  Length 146;
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                                                                                                                                  Indels
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
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                                                                                                                                    Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 2000000000
   48
 100.0
                                                Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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48
1 NGWYPW 6
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1: /cgn2_6/ptodata/1/paa/I
2: /cgn2_6/ptodata/1/paa/I
3: /cgn2_6/ptodata/1/paa/I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                               /cgn2_6/ptcdata/1/paa/US097A_COMB.pep:*
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/cgn2_6/ptcdata/1/paa/US09B_COMB.pep:*
/cgn2_6/ptcdata/1/paa/US09B_COMB.pep:*
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/cgn2_6/ptcdata/1/paa/US100_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US084_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US06_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US089_COMB.pep:*
/cgn2_6/ptodata/1/paa/US099_COMB.pep:*
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 US-09-075-338C-32
US-09-300-425B-32
                                                                                                     SUMMARIES
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                                                Description
Sequence 32, Appl
Sequence 32, Appl
                                                                                                                                                                                                                                                                                                                                                                                        US-09-075-338C-32
                                                                                                                                SOFTWARE: P
SEQ ID NO 32
LENGTH: 6
TYPE: PRT
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                         FILE REFERENCE:
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100.0%;
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uenc uenc uenc ence ence ence	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	equence 32, App equence 78362,

## ALIGNMENTS

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; ORGANISM: Artificial Sequence; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B; OTHER INFORMATION: antibody clone
US-09-075-338C-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32, Application US/09075338C GENERAL INFORMATION:
APPLICANT: MERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/075,338C CURRENT FILING DATE: 1998-05-11 NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BIRCHLER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
Score 48; DB 14;
Pred. No. 5.2e+06;
                           Length 6;
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Matches

Conservative

Mismatches

Indels

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US-09-512-082-32
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SEQ ID NO 32
LENGTH: 6
Query Match
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LENGTH: 6
TYPE: PRI
ORGANISM: Artificial Sequence
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APPLICANT: VITI, FRANCESCA
APPLICANT: VITI, FRANCESCA
APPLICANT: BIRCHLER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: AUGUSTIANING THEM AND THERAPBUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: AUGUSTIANING THEM AND THERAPBUTIC METHOD FOR TREATMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
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CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1999-04-28
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CURRENT APPLICATION NUMBER: US/09/512,082
CURRENT FILING DATE: 2000-02-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                OTHER INFORMATION:
                                                                                                   ORGANISM: Artificial Sequence FEATURE:
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OTHER INFORMATION:
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nes 6; Conserv
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VITI, Francesca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09300425B
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NERI, Dario
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                                                                Description of Artificial Sequence: anti-ED-B antibody clone
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                                                                                                                                                                                                                              1998-05-11
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100.0%; Pred. No. 5.
tive 0; Mismatches
            100.0%;
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            Score 48;
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            DB
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            19;
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Query Match
Best Local Similarity
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US-09-791-537-78362
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                                                                                                                                                              ; SEQ ID NO 7581
; LENGTH: 318
; TYPE: PRT
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 78362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7581, Application US/10156761
                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                         APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 23
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TIPLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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APPLICANT: IKEDA, HARUO
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106 SGWYPW 111
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                                1 NGWYPW 6
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HORIKAWA, HIROSHI
                                                            Conservative
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                                                              Score 43; DB 27;
Pred. No. 4.2e+02;
1; Mismatches 0
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; Mismatches 0;
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                                                                                              DB 27;
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RESULT 6

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FITLE OF INVENTION:
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/10/419,128
CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16759
LENGTH: 115
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                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Pseudomonas aeruginosa US-10-419-128-16759
                                                                                                                                                              US-10-437-963-144814
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GENERAL INFORMATION:
APPLICANT: MATC J. RUBENfield et al.
APPLICANT: INVENTION: NICLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                         Sequence 144814, Application US/10437963 GENERAL INFORMATION:
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Best Local
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SEQ ID NO 261895
LENGTH: 58
TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                     APPLICANT:
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APPLICANT: Kovalic David K
                                                                                                         APPLICANT: La Rosa, Thomas
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                                                                                                                                                                                                                                      56 GWYPW 60
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5; Conserve
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5; Conserv
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                                                                           Kovalic, David K. Zhon v<sup>4</sup>L...
                                                                    Zhou, Yihua
Barbazuk, Brad
               Boukharov, Andrey A.
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                                                 Yongwei
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100.0%;
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Pred. No.
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1.5e+02;
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated Wit
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT EDILICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 144814
LENGTH: 179
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SOFTWARE: CUSTOM
SEQ ID NO 3650
LENGTH: 562
TYPE: PRT
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Best Local Similarity
                                                  APPLICANT: Cao Yongwel
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 203-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191909
                                                                                                                                                                                                                                                                               Sequence 191909,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILE REFERENCE: 21272-049 CURRENT APPLICATION NUMBER: PCT/US01/08631 CURRENT FILING DATE: 2001-03-30
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                                                                                                                                                                                                     APPLICANT:
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ORGANISM: Glycine max
                     TYPE: PRT
                                      ENGTH:
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les 5; Conserv
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Kovalic David K
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b; Pred. No. 9.3
0; Mismatches
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. 3.6e+02;
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9.3e+
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FEATURE:

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Best Local Similarity
"hes 5; Conserv:
                                                 ; ORGANISM: Anopheles gambiae PCT-US02-28315-76
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 Query Match
Best Local Similarity
                                                                                 SOFTWARE: PatentIn version 3.0 SEQ ID NO 76 . LENGTH: 393 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                              Sequence 76, Applica GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191881
LENGTH: 219
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GENERAL INFORMATION
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PRIOR FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 97
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: PCT/US02/28315
CURRENT FILING DATE: 2002-09-04
                                                                                                                                                                                                                              APPLICANT: KIOŚS, Briań
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF INSECT Or83B ODORANT RECEPTOR
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 10657-005-228
                                                                                                                                                                                                                                                                                                                             APPLICANT:
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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ORGANISM: Glycine max
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Kloss, Brian
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83.3%;
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Score 40;
Pred. No.
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Pred. No.
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Pred. No.
; DB 1;
. 1.4e+03;
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7.9e+02;
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           Length 393;
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RESULT 15
US-10-183-708-92
Sequence 92, Application US/10183708
GENERAL INFORMATION:
APPLICANT: VOSSHALL, LESLIE
APPLICANT: AMREIN, HUBERT
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Best Local Similarity
"~+~hes 5; Conserv?
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; TYPE: PRT
; ORGANISM: Drosophila Melanogaster
US-09-932-227-92
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Best Local Similarity
Them 5; Conserv.
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US-09-799-131-92
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 92
LENGTH: 403
TYPE: PRT
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APPLICANT: AMREIN, HUBERT
APPLICANT: AXEL, RICHARD
APPLICANT: AXEL, RICHARD
TITLE OF INVENTION: GENES ENCODING INSECT ODORANT RECEPTORS AND USES THEREOF
FILE REFERENCE: 0575/58715-A-PCT-US/JPW/ADM/BJA
CURRENT FILING LOTE: 2001-08-17
CURRENT FILING LOTE: 2001-08-17
CURRENT FILING LOTE: 2001-08-17
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PRIOR FILING DATE: 2000-02-25
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CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION OF THE PRIOR APPLICATION OF T
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APPLICANT: AMREIN,
APPLICANT: AXEL, R:
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## APPLICANT: AXEL, RICHARD
## TITLE OF INVENTION: GENES ENCODING INSECT ODORANT
## CILE REPERENCE: 0575/58715-AA-PCT-US/JPW/ADM/BJA
CURRENT APPLICATION NUMBER: US/10/183,708
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 09/932,227
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 1999-02-25
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Minimum DB seq
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compus
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US-10-286-897-6025
US-10-286-897-6025
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US-10-283-244-8518
US-10-283-244-1550
US-10-293-244-3518
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Sequence 6716, Ap	Sequence 29, Appl	Sequence 39, Appl	Sequence 1137, Ap		Sequence 100, App	Sequence 1138, Ap	Sequence 1772, Ap	Sequence 5399, Ap	Sequence 1545, Ap	Sequence 3, Appli	Sequence 18, Appl	Sequence 17, Appl	Sequence 7981, Ap	Sequence 24, Appl	Sequence 166, App	•	Sequence 10, Appl	Sequence 1442, Ap

## ALIGNMENTS

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SEQ ID NO 37 LENGTH: 552

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CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 878
LENGTH: 258
TYPE: PRT
RCANISM: Homo sapiens
US-10-408-765A-878
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US-10-408-765A-2774
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Query Match
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Best Local Similarity
Watches 6; Conservat
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APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradfor
APPLICANT: Taylor, Steven
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LENGTH: 512
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                                                                                                                                                                                                           APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 GWHPW 248
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                                                                                                                                                                                                                                                                                                                                         Zhang, Bing
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85.7%;
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Pred. No. 1.2e+02;
            Score 36;
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Pred. No. 1
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            DB 6;
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1.1e+02;
            Length 258;
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RESULT 7
PCT-US03-07174-20
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1572
; LENGTH: 258
; TYPE: PRT
; ORGANLEM: Homo sapiens
US-10-408-765a-1572
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; LENGTH: 330
; TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
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Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/128,706
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/09/543,681 PRIOR FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/603,114
CURRENT FILING DATE: 2003-06-24
                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRATITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WAIDOCK, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEILE REFERENCE: 660088.465
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Taylor, Steven W.
Glenn, Gary M.
                                                                                                                                ilarity 100.0%;
Conservative (
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                                                                                                                                                  75.0%; Score 36; 100.0%; Pred. No.
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hes 0;
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APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (5373)A
CURRENT APPLICATION NUMBER: US/10/612,783
CURRENT FILING DATE: 2003-07-02
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Best Local
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Best Local Similarity
Matches 4; Conserv
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                                      NUMBER OF SEQ ID NOS: 7098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(5373)A CURRENT APPLICATION NUMBER: US/10/612/783 CURRENT FILING DATE: 2003-07-02 NUMBER OF SEQ ID NOS: 7098
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CURRENT APPLICATION NUMBER: PCT/US03/07174
CURRENT FILING DATE: 2003-05-12
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TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 10/094,240 PRIOR FILING DATE: 2002-03-08 NUMBER OF SEQ ID NOS: 27
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PPLICANT: Kovalic, David K.
PPLICANT: Zhou, Yihua
PPLICANT: Cao, Yongwei
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TYPE: PRT
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                                                                                                                        Other Molecules
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SOFTWARE: Pt_r;
SEQ ID NO 2453
FENGTH: 634
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                                                                                                                               Sequence 2453, Application US/10258898A GENERAL INFORMATION:
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Matches 4
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GENERAL INFORMATION:
                 CURRENT APPLICATION NUMBER: US/10/258,898A CURRENT FILING DATE: 2002-10-29 PRIOR APPLICATION NUMBER: US/09/488,725 PRIOR FILING DATE: 2000-01-21
                                                                                APPLICANT: Hyseq Inc
TITLE OF INVENTION: NOVE
FILE REFERENCE: 784FLPCT
PRIOR APPLICATION NUMBER: US09/552,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
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100.0%;

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Mismatches

Indels

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Gaps

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1.9e+02

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PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/09/552,317
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/286,897 CURRENT FILING DATE: 2002-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Novel Nucleic Acid and
                                                                    ORGANISM: Homo sapiens
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LOCATION: (1)..(481)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/693,036
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/662,191 FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/653,450
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US-10-258-898A-2453
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US-10-408-765A-2458
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APPLICANT: BAUGHN, MARIAH R.

TITLE OF INVENTION: AMINOACYL TRNA SYNTHETASES
FILE REFERENCE: PI-0323 PCT
CURRENT APPLICATION NUMBER: US/10/450,727
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: 60/255,963
PRIOR APPLICATION NUMBER: 60/255,963
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2
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SEQ ID NO 2453
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Best Local (
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PRIOR APPLICATION NUMBER: US09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: US09/693,036
PRIOR FILING DATE: US09/727,344
PRIOR FILING DATE: 2000-11-29
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PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US09/653,450
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                                                            APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
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                APPLICANT:
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LENGTH: 1(
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Gibson, Bradford W. Taylor, Steven W. Glenn, Gary M.
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; ORGANISM: Homo sapiens
US-10-408-765A-2458
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US-10-286-897-6025, Application US/10286897
Sequence 6025, Application US/10286897
GENERAL INFORMATION:
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US-10-258-898A-6025
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Sequence 6025, Application US/10258898A
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
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SOFTWARE: pt_FL_genes_b
SEQ ID NO 6025
LENGTH: 1291
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NUMBER OF SEQ ID NOS: 3077
SOFTMARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/286,897 CURRENT FILING DATE: 2002-11-01
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CURRENT APPLICATION NUMBER: US/10/258,8981

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## ALIGNMENTS

C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: H64236
A;Status: preliminary; nucleic acid sequence not shown; translation not shown hypothetical protein MG333 - Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 19-May-2000 C;Accession: H64236 R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleis: M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A. RESULT H64236 Query Match
Best Local Similarity
"~+~hes 5; Conserv Š C; Superfamily: acyl carrier protein phosphodiesterase 밁 A; Genetic code: SGC3 A;Cross-references: GB:U39715; GB:L43967; NID:g1046026; PID:g1046036; TIGR:MG333 A;Experimental source: strain G-37 A; Molecule type: DNA A; Residues: 1-126 < TIGR> Genetics: 68 2 GWYPW 6 GWYPW 72 Conservative 87.5%; Score 42; pred. No. 0 Mismatches 9; 8d <u>ب</u> 0, Length 126 Clayton, R.A.; Fleischmann, R. D.M.; Phillips, C.A.; Merrick, Indels 0 Gaps 0

RESULT S73688

hypothetical protein HI1366 - Mycoplasma pneumoniae (strain ATCC 29342) N;Alternate names: hypothetical protein PO1\_orf197

C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb\_1997 #sequence\_revision 25-Apr-1997 #text\_change 17-Mar-2000

B.C.; Herrmann,

C;Accession: S73688
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, Nucleic Acids Res. 24, 4420-4449, 1996.
A;Title: Complete sequence analysis of the genome of the bar A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73688 bacterium

Mycoplasma pneumon

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;NoLecule type: DNA A;NoLecule type: DNA A;NoLecule type: The Notes: 1-197 (HIM) A;Residues: 1-197 (HIM) A;Cross-references: EMBL:AE000034; GB:U00089; NID:g1674031; PIDN:AAB96010.1; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Novem

A; Note: the C; Genetics:

C;Superfamily: acyl carrier protein phosphodiesterase Genetic code: SGC3

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hypothetical protein [imported] - Brevibacterium linens c;Species: Brevibacterium linens C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text C;Accession: T51117
                                                                                                           RESULT 5
T51117
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S72858
                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein B2126_C2_219 - Myo
;Species: Myoobacterium Leprae
C;Date: 19-Mar-1997 #sequence_revision
C;Accession: S72858
R;Smith, D.R.; Robison, K.
Mol. Gen. Genet. 263, 423
A; Title: A carotenogenic
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                                                                                                                                                                                                                                                                                     A; Molecule type: DNA A; Residues: 1-336 <SMI>
                                                                                                                                                                                                                                                                                                                                         A; Description: Mycobacterium A; Reference number: $72585
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A; Cross-references: GB: AL445566; PID: g14089726;
A; Cross-references: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-198 < K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: H90550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein MYPU_3120 [imported] - Mycoplasma pulmonis (strain UAB C;Species: Mycoplasma pulmonis C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U00017; NID:g466994; PIDN:AAA17198.1; PID:g467013
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                                                                                                                                                                                                                                                                                                                            A; Accession:
                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library,
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Matches 5
                                    Krubasik, P.; Sandmann,
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Pred. No.
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Pred. No.
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Pred. No.
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           Brevibacterium
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RESULT 7
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S55490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; MOLECULE VIFT
A; Residues: 1-456 < KRU>
A; Cross-references: EMBL: AF139916; PIDN: AAF65580.
A; Cross-references: DSM 20426; ATCC9175
                                                                                                                                                          A; Cross-references: EM A; Experimental source:
                                                                                                                                                                                                                                    A; Reference number: A; Accession: T22377
                                                                                                                                                                                                                                                     A; Reference number: 219556
                                                                                                                                                                                                                                                                                                  C;Species: Caenorhabditis
C;Date: 15-Oct-1999 #seque
C;Accession: T22377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SPAC5H10.12c - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 31-Jan-2000 C;Accession: T38976; S55490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: Z25303; MUID:20279196; PMID:10821176
A;Accession: T51117
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                        A; Map position:
                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-708 <WIL>
                                                                                                                                                                                                          A;Molecule
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                                                                                                                                                                                                                                                                                      R; Wild,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-371 <CO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: T38976
                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F48C11.2 - Caenorhabditis elegans
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Best Local
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                             Similarity
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NGWYPW 6
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                                                                                           115/3; 149/1; 305/2;
                               Conservative
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                                                                                                                                                                         EMBL: 280789;
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                                                                                                                                                        BL:280789; PIDN:CAB02551.1; clone F48C11
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83.3%;
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brary, May 1995
                          Score 39; DB 2;
Pred. No. 1.3e+02;
0; Mismatches 1
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Pred. No.
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                                                                                           547/2;
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696 NGWKPW 701

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R;She,
                                                                      hypothetical protein SSO1052 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: E90257
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Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712
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A;Cross-references: EMBL:AL021730; PIDN:CAA16831.1; GSPDB:GN00067; SPDB:SPBC4C3.09
A:Experimental source: strain 972h-; cosmid c4C3
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A;Residues: 1-376 <W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: Z21910
A;Accession: T40488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; submitted to the EMBL Data Library, February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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C; Superfamily: pectinesterase
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A; Residues: 1-223 <STO>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A86141; A; Accession: A86249
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status:
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Best Local
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       Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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4; Conserv
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80.0%;
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Pred. No.
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Pred. No. 61;
1; Mismatches
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1e+02;
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1998
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   Y.; Allard, G.; Awayez, M.J.; Cha
Peng, X.; Thi-Ngoc, H.P.; Redder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                 Chan
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C; Function:
A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                              cellulase (EC 3.2.1.4) H precursor - Clostridium thermocellum N; Alternate names: endo-1,4-beta-glucanase; endoglucanase H C; Species: Clostridium thermocellum C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_chance; Accession: JH0157 R; Yaguee, E.; Beguin, P.; Aubert, J.P. Gene 89, 61-67, 1990 .

A; Title: Nucleotide sequence and deletion analysis of the cell
                                                                                                                  A;Cross-references: GB:M31903; NID:g144773; PIDN:AAA23225.1; PID:g144774 A;Note: the authors translated the codon CAG for residue 863 as His C;Comment: Cellulase H is involved in the hydrolysis of cellulose and ar C;Comment: Cellulase H hydrolyzes carboxymethylcellulose, p-nitrophenyl-
                                                                                                                                                                                                                                                                                                                                    A;Reference number: JH0157; MUID:90323606; PMID:2197182 A;Accession: JH0157
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JH0157
                                                                      A;Gene: celH
                                                                                                       C; Genetics:
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A; Residues: 1-900 < YAG>
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hydrolysis

of

1,4-beta-D-glucosidic linkages

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beta-D-glucans such

as

ellulose and arranged in cel p-nitrophenyl-beta-D-cellob

31-Dec-1991 #text\_change

15-Oct-1999

cellulase-encoding

gene

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A; Molecule type: DNA
A; Residues: 1-540 <570>
A; Cross references: GB:AE004836; GB:AE004091; NID:g9950405; PIDN:AAG07585.1;
A; Experimental source: strain PAO1
C; Genetics:
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                                                                                                                            A; Gene:
                                                                                                                                                                                                                               A;Title: Complete genome se
A;Reference number: A82950;
A;Accession: B83121
                                                                                                                                                                                                                                                                             R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.; (Lory, S.; Olson, M.V.; Lory, S.; Olson, M.V.; Pham, M. (Lory, S.)
                                                                                                                                                                                                                                                                                                                                                  probable AMP-binding enzyme PA4198 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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B83121
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A; Residues: 1-764 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene:
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                                                                             Best
                                                                                            Query Match
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                                                               Matches
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Best Local
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235 NGWCYPW 241
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                              1 NGW-YPW 6
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                                                            Similarity
6; Conserv
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                                                                                                                                                                                                                                              sequence of Pseudomonas aeruginosa 50; MUID:20437337; PMID:10984043
                                                                          78.1%;
85.7%;
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                                                          Score 37.5; I
Pred. No. 1.76
0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                            Coulter,
                                                                                                                                                                                                                                                                                                        A.L.; Mizoguchi, S.D.;
Coulter, S.N.; Folger, I
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1.9e+02;
0;
                                                                        DB 2;
L.7e+02;
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                                                                                     Length 540;
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                                                       Gaps
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Larbig,
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A;Pathway: cellulose degradation C;Superfamily: Clostridium cellulase repeat homology C;Keywords: glycosidase; hydrolase; polysaccharide degre;1-44/Domain: signal sequence #status predicted <SIG>F;45-900/Product: cellulase H #status predicted <CEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;309-324/Region: proline/serine/threonine-rich
F;631-654/Region: proline/serine/threonine-rich
F;633-856/Domain: Clostridium cellulase repeat homology <CCR1>F;872-895/Domain: Clostridium cellulase repeat homology <CCR2>
                                                                                                                                                                                                                                                                                                                                                            R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, May 1999
A;Reference number: Z21609
A;Accession: T36541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Guillen, G.; Lea1, M.O., (LL. L. L. March 199 submitted to the EMRL Data Library, March 199 more resistance of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outer membrane protein class 5c - Neisseria meningitidis (fragment)
C;Species: Neisseria meningitidis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
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S43104
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RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SCH1029c1 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T36541
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A;Molecule type: DNA
A;Residues: 1-250 <GUI>
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A; Residues: 1-262 <MUR>
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A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local :
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Best Local
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                                                                                141 GWHPW 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G.; Leal, M.J.; Alvarez, A.; Delgado, M.; Silva, R.; Herrera, L.
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outer membrane protein class 5C precursor - Neisseria meningitidis (strain Z3476) C;Species: Neisseria meningitidis (C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
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A;Title: Cloning and expression in Escherichia coli of opc, the gene A;Reference number: A44611; MUID:92261288; PMID:1813777
A;Accession: A44611
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Search completed: August 20, Job time: 5.19277 secs
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A; Cross-references: GB:M80195
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SEQUENCE OF 1-47 FROM N.A.  STRAIN-ATCC 33530 / G-37;  STRAIN-ATCC 33530 / G-37;  REDLINE-94075230; PubMed-8253680;  Peterson S.N., Hu PC., Bott K.F., Hutchison C.A. II  Peterson S.N., Hu PC., Bott K.F., Hutchison C.A. II  Peterson S.N., Hu PC., Bott K.F., Hutchison C.A. II  REPLIANCE OF THE MYCOPLASMA GENITALIUM GENOME by usin  sequencing.";  J. Bacteriol. 175:7918-7930(1993).  [3]  CONCEPTUAL TRANSLATION.  Bairoch A.;  Unpublished observations (FEB-1997).	RP SEQUENCE FROM N.A.  RC STRAIN-ATCC 33530 / G-37;  RX MEDLINE-96026346; PubMed-7569993;  RX MEDLINE-96026346; PubMed-7569993;  RX Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,  RA Fritchmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.  RA Fritchman J.L., Weidman J.F., Sandla K.V., Sandusky M., Fuhrmann  RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick  RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick  RA Tomb JF., Dougherty B.A., Bott K.F., Hu PC., Lucier T.S.,  Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;  "The minimal gene complement of Mycoplasma genitalium.";  Science 270:397-403(1995).	D_MYCGE STANDARD; PRT; 196 AA.  ACPD_MYCGE STANDARD; PRT; 196 AA.  P47575; 049357; 01-FEB-1996 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update) Putative acyl carrier protein phosphodiesterase (EC phosphodiesterase).  Mycoplasma genitalium: Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; NCBI_TaxID-2097;	35 72.9 2195 1 SC16_YEAST 34 70.8 167 1 REV_VILV 6 34 70.8 167 1 REV_VILV 6 34 70.8 167 1 REV_VILV 7 34 70.8 176 1 Y069_TREPA 8 34 70.8 181 1 AAC2_MYCTU 9 34 70.8 186 1 RBB9_HOUSE 1 34 70.8 186 1 RBB9_MOUSE 1 34 70.8 186 1 RBB9_EAT 2 34 70.8 195 1 AAC2_MYCFO 3 34 70.8 239 1 PNUC_ECOLI 3 34 70.8 239 1 LCAT_ELIQU 5 34 70.8 299 1 LCAT_ELIQU 5 ALIGNMENTS
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HAMAP; MF_01216; -; 1.

Interpro; IPR003680; NADHdh_2.

Pfam; PF02525; Flavodoxin_2; 1.
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CONFLICT 44 47 NELP -> MNYQ (IN REF. 3).

SEQUENCE 196 AA; 22076 MW; 9D26C167A3DBC8BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -I- FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of the phosphopantetheine prosthetic group from ACP (By similarity).
-I- CATALYTIC ACTIVITY: Holo-[acyl-carrier protein] + H(2)0 = 4'-phosphopantetheine + apo-[acyl-carrier protein].
-I- SIMILARITY: Belongs to the acpD family.
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01-NOV-1997 (Rel. 35,
28-FEB-2003 (Rel. 41,
Putative acyl carrier
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Hypothetical protein; Hydrolase;
SEQUENCE 197 AA; 21550 MW; B
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HAMAP; MF_01216; -; 1.
InterPro; IPR003680; NADHdh_2
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STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
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                                                                                                                                                                          GWY PW
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          STANDARD;
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Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                              0;
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Pred. No
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          PRT;
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                                                                                                                                                                                                                                                                                                                                                 ŏ.
             198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restriong as its content in over the content over the content of the
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5.6;
                                                                                                                                                                                                                                                                                                                                              DB 1;
5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pirkl E.,
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                                                                                                                                                                                                                                                                                                                                                                                 Length 197;
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RESULT 4

OG9A_D

OG9A_D

AC P82985

AC P82985

DT 16-CCT

DT 16-CCT

DT 16-CCT

DT 28-FEB

DE Putati

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GN OR69A,

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OC Neopte

CO Neopte

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RP STRAIN

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Best Local S
Matches 5
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28-FEB-2003 (Rel. 41, I
28-FEB-2003 (Rel. 41, I
Putative acyl carrier I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.
Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
-!- FUNCTION: Converts holo-ACP to apo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21267165; PubMed=11353084; Chambaud I., Heilig R., Ferris S., Bandszer I., Dybvig K., Wroblewski H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N. STRAIN=UAB CTIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYPU_3120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphodiesterase).
                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Inso
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                          P82985,
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; H90550; H90550.
MypuList; MYPU_3120;
HAMAP; MF_01216; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
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                                                                                                                                                                                              Putative odorant receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
SEQUENCE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003680; NADHdh_2.
Pfam; PF02525; Flavodoxin_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blanchard A.;
                                                                          SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID=7227;
                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                                                                                    069A_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL445564; CAC13485.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of the phosphopantetheine prosthetic group from ACP (By similarity). CATALYTIC ACTIVITY: Holo-[acyl-carrier protein] + H(2)O = 4'-phosphopantetheine + apo-[acyl-carrier protein]. SIMILARITY: Belongs to the acpD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                           139 GWYPW
                                                                                                                                                                                                                                                                                                                                                                     2 GWYPW
                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            il protein;
198 AA; 2;
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            n; Hydrolase; Complete proteome 22673 MW; 453B99E001609FD4 CR
                                                                                                                                                                                                                                                                                                                                                                                                                  87.5%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
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protein phosphodiesterase
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                                                                                                                                                                  (Fruit fly).
                                                                                                                                                                                                          sequence update)
annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 4
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               453B99E001609FD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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  Viari A.,
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                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
5.6;
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A
                                                                                                                                      Insecta; Pterygota; era; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Samson I
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a E.P.C.,
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      S.F.
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E
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A Wan K.L., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.M., RA Beeson K.Y., Denos P.V., Berman B.P., Bhandari D., Bolshakov S.M., Borchan M.R., Bouck J., Bhandari D., Bolshakov S.M., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Fleischmann W., RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibegwam C., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Menkolov G., Milahina N.V., Mobarry C., Mozris J., Moshrefi A., Merkolov G., Milahina N.V., Mobarry C., Mozris J., Moshrefi A., N., Nixon K., Nusskern D.R., Pancleb J.M., RA Rainert K., Ramington K., Saunders R.D.C., Scheeler E., Shen H., Ra Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Ra Rainert K., Ramington K., Saunders R.D.C., Scheeler E., Shen H., Ra Sheng X.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ra Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Pitcher E., Wang S., Pan S., Yao Q.A., Pan S., Pan S.,
                                                                                                                                                                                                 DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as wing modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                    Hypothetical Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                 EMBL; AE003539; -; NOT_ANNOTATED_CDS
FlyBase; FBgn0041622; Or69a.
InterPro; IPR004117; 7tm_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished observations (MAY-2001).
-I- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sutton G
Brandon
                                    TRANSMEM
                                                                     TRANSMEM
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                    DOMAIN
                                                                                                                                             TRANSMEM
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                                                                                                                                                                                                                                                   ycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO FAMILY DR-OR OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTORS
                                                                                                                                                                                                                                                                                    PF02949; 7tm_6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>.</u>
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R.C., Rogers Y.-H.C., Blazej R.G
40
61
70
91
139
160
220
230
230
270
270
306
                                                                                                                                                                                                                                                                   protein;
 S Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
1 A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
1 Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                   Multigene
                                                                                                       3 (POTENTIAL).
CYTOPLASMIC (PC
4 (POTENTIAL).
                                                                                                                                        1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (
5 (POTENTIAL).
                                 5 (POTENTIAL).
CYTOPLASMIC (F
 EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
                                                                       EXTRACELLULAR 5 (POTENTIAL)
                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                               G-protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                   (POTENTIAL).
                                                                                                                     (POTENTIAL).
                                                                                                                                                                                             (POTENTIAL).
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                                                                                    (POTENTIAL
                                                                                                                                                          (POTENTIAL)
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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Richterford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA River R., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Golibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lous R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
RA Charley H., Seyery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880(2002)

CC - Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
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or send a
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C5H10.12c in chromosome
SPAC5H10.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q09680;
01-NOV-1995
01-NOV-1995
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                        between the Swiss Institute of Bioinformat:
the European Bioinformatics Institute. Then
use by non-profit institutions as long a
modified and this statement is not removed.
                                                                                EMBL; Z49811; CAA89962.1; PIR; T38976; S55490.
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                             Nature 415:871-880(4004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood V., Gwilliam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                   s requires a license agreement (S an email to license@isb-sib.ch).
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Pred. No.
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N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
EC1EFBB19115362C CRC64;
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                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB
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GeneDB\_SPombe;

ombe; SPAC5H10.12c; IPR002495; Glyco\_t

Glyco\_transf\_8; 1.

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GUNELCO T
GUNELCO T
AC P16218
DT 01-APR
DT 01-APR
DT 28-FEB
DE Endogl
DE (Cellu
GN CELH.
OS Clostr
OC Bacter
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PME_DAUCA
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Best Local :
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                                                                                      GUNH_CLOTM STANDARD; PR
P16218;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seque
28-FEB-2003 (Rel. 41, Last annot
Endoglucanase H precursor (EC 3.
Bacteria;
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ACT_SITE
SEQUENCE
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                                   Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21960069; PubMed-11964128;
Markovic O., Cederlund E., Griffiths W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; eudicotyledons; core
Asteridae; campanulids; Apiales; Apiaceae; Daucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Pectinesterase (EC 3.1.1.11) (Pectin methylesterase)
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P83218;
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                                                                        (Cellulase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-structure.
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CATALYTIC ACTIVITY:
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                  248
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Pro; IPR000070; Pectinesterase.
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                                                                                                                                                                                                                                                                                                                                                                               Similarity
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PS00503; PECTINESTERASE_2; 1.
ie; Aspartyl esterase; Cell wall;
                                                                                                                                                                                                                                                                                  GWFPW
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                 Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
136
157
                                   thermocellum.
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                                                                                                                                                                                                                                                                                                                                                         Conservative
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157
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66.7%;
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3 POTENTIAL.
3688 MW; 890BAD4A0E66379B CRC64;
                 Clostridia;
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TO THE PECT
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(EC 3.2.1.4)
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                   Clostridiales;
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                                                                                          (EGH) (Endo-1,4-beta-glucanase)
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                   Clostridiaceae;
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RESULT 8
BPT1\_YEAST
ID BPT1\_Y
AC P14772
DT 01-APR
DT 01-NOV
DT 15-SEP

STANDARD;

PRT;

1559

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BPT1\_YEAST P14772; 01-APR-1990 01-NOV-1997 15-SEP-2003

(Rel. 14, Created)
(Rel. 35, Last sequence up)
(Rel. 42, Last annotation

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90323606; PubMed=2197182; Yaguee E., Beguin P., Aubert J.-P.; Yaguee E., Beguin P., Aubert J.-P.; "Nucleotide sequence and deletion analysis gene celh of Clostridium thermocellum."; Gene 89:61-67(1990).
                                                                                                                                                 DOMAIN
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DOMAIN
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MEDLINE=90323606;
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NCBI_TaxID=1515;
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InterPro; IPR001547; G.
Pfam; PF03425; CBM_11;
                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                             InterPro;
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SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYCOSYL HYDROLASES.
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 133
                                                                                                                                                                                                                                                 PF00404;
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                                                                                                                                                                                                                                                            PF00150;
             1 NG-WYPW
                                        6; Conserv
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                                                                                                                                                                                                                 PS00448; CLOS_CELLULOSOME_RPT; PS00659; GLYCOSYL_HYDROL_F5; 1
                                                                                                                                                                                                                                      PS00018; EF_HAND; UNKNOWN_1.
 NGDWYPW 139
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IPR002105;
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85.7%;
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Glyco_hydro_5.
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CATALYTIC (BY SIMILARITY).
CATALYTIC (BY LINKER).
PRO/THR-RICH (LINKER).
CELLULOSE-BINDING (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
2 X 24 AA APPROXIMATE REPEATS.
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                                                     Pred.
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RC STRAIN-S288C / AB972;

RX MEDLINE-97313267; PubMed-9169871;

RA JOHNSTON M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,

RA JOHNSTON M., Hillier L., Riles L., Dubols E., Duesterhoeft A.,

RA Benes V., Brueckner M., Delius H., Dubols E., Duesterhoeft A.,

RA Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,

RA Entian K.-D., Floeth M., Goffeau A., Hebling W., Koetter P.,

RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,

RA Louis E.J., Messenguy F., Mewes H.-W., Mlosga T., Moestl D.,

RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,

RA Mueller-Auer S., Nentwich U., Obermaier B., Rieger M., Rinke M., Rose M.,

RA Mueller-Auer S., Nentwich B., Scholler P., Schwarz S.,

RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,

RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,

RA Vlarendeels F., Voet M., Volkaert G., Voss H., Wambutt R., Wedler E.,

RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";

RA Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wiosga T., Zimmermann F.K.;
"Sequence analysis of the CEN12 region of Saccharomyces cerevisiae
a 43.7 kb fragment of chromosome XII including an open reading fram
homologous to the human cystic fibrosis transmembrane conductance
regulator protein CFTR.";
Yeast 12:693-708(1996).
                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20253522; PubMed-10790694; Petrovic S., Pascolo L., Gallo R., Cupelli F., Ostrow J Goffeau A., Tiribelli C., Bruschi C.V.; "The products of YCF1 and YLL015w (BPT1) cooperate for dependent vacuolar transport of unconjugated bilirubin Saccharomyces cerevisiae."; Yeast 16:561-571(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-245 FROM N.A.

MEDILINE-89306677; PubMed-2545538;

Boy-Marcotte E., Damak F., Camonis J., Garreau H., Jacquet M.;

"The C-terminal part of a gene partially homologous to CDC 25 suppresses the cdc25-5 mutation in Saccharomyces cerevisiae.";

Gene 77:21-30(1989).
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Purnelle B., Goffeau A.;
"The sequence of 32kb on the left arm of yeast chromosome XII reveals six known genes, a new member of the seripauperins family and a new ars transporter homologous to the human multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bile pigment transporter 1.

BPT1 OR YLL015W OR L1313.

Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Cooperates
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CAA66162.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for the ATP-dependent vacuolar transport
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C.V.;
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RESULT 9 Y017\_METJA ID Y017\_METJA

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GO; GO:0015127; F:bllirubin transporter actty
GO; GO:0015886; F:cadmium ion transporter actty
GO; GO:0015723; P:bllirubin transport; IGI.
GO; GO:0015723; P:cadmium ion transport; IDA.
InterPro; IPR003593; AAA_ATPase,
InterPro; IPR00140; ABC_TM_transpt.
InterPro; IPR003439; ABC_transporter.
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SMART; SM00382; AAS, 2.
SMOSITE; PS00211; ABC_TRANSPORTER_1;
PROSITE; PS50893; ABC_TRANSPORTER_2;
                                                                                                                                                                                                                                                                                 TRANSMEM
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Pfam; PF00005; ABC_tran; 2.
ProDom; PD000006; ABC_transport
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EMBL; X9148B; CAA62776.1;
EMBL; M26647; AAA16564.1;
PIR; S64757; S64757.
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5; Conserv
NGWYP 217
                             NGWYP 5
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F:bilirubin transporter activity; IGI
F:cadmium ion transporter activity; II
                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e; Glycoprotein; Transport.
LUMENAL (BY SIMILARITY).
1 (BY SIMILARITY).
1 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
2 (BY SIMILARITY).
LUMENAL (BY SIMILARITY).
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LUMENAL (BY SIMILARITY).
7 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
8 (BY SIMILARITY)
                                                             Score 37; DB Pred. No. 2e+ 0; Mismatches
                                                               0
                                                                                                                                                               ATP
                                                                                                                                                                                                                                           LUMENAL (BY SIMILARITY).
15 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
16 (BY SIMILARITY).
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9 (BY SIMILARITY)
CYTOPLASMIC (BY S
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5 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
6 (BY SIMILARITY).
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CYTOPLASMIC (BY SIMILARITY).
4 (BY SIMILARITY).
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13 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).
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17 (BY SIMILARITY).
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                                                                                                                                O460F3561E3125D5
                                                                                                                                                                 (POTENTIAL)
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2e+02;
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                                                                                            Length 1559
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RESULT 10
YE66_MCTJA6
ID 01-N(
DT 01-N(
DT 28-F)
DE HYPO
GN MJ14
OS Meth
OC Arch
OX NCB:
RN [1]
RP SEQ
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01-NOV-1997
28-FEB-2003
MEDIINE-6637999; PubMed-8688087;
MEDIINE-66337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Button G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Kerlavage A.R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
                                                                                                                                                                                                                                  Q58861;
01-NOV-1997
01-NOV-1997
28-FEB-2003
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Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschil.";
Science 273:1058-1073(1996).
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Archaea; Euryarchaeota; Methanocaldococcaceae; Me
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                                                                                                                                                                                                                                                                                                            METJA
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                                                                                                 STRAIN-JAL-1
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                      Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
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MEDLINE=96337999; I
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                                                                                                                                          NCBI_TaxID=2190;
                                                                                                                                                                                                                    Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00665; rve; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 214 AA; 25506 MW; 0F135E2C748F933D CRC64;
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                                                                                                                                                                                                                                                                                            YE66_METJA
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PF00665; rve;
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PubMed=8688087;
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35, Last sequence update)
41, Last annotation update)
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                                                                                               / ATCC
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                                                                                                                                                                                                                                                                                            PRT;
                                                                                               43067;
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RESULT 11
R18B_MOUSE
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H. Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        099N84; Q9CRKO; Q9DCR8;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
28S ribosomal protein S18b, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come titles requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
STRAIN=C57BL/6J; TISSUE=Embryonic stem
MEDLINE=21085660; PubMed=11217851;
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PIR; /
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                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-21413863; PubMed-11402041;
Suzuki T., Terasaki M., Takemoto-H
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; SEQUENCE 214 AA; 2:
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                                                                                                                                                                                                                                                       Identification J. Biol. Chem.
                                                                                                                                                                                                                                                                                                    Watanabe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome jannaschii.";
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A64483; A64483.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 WYPW 149
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[LARITY: STRONG, TO
                                                                                                                                                                             Shinagawa A., Shibata K.,
                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
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Rodentia;
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3C6D5A76051F17EB CRC64;
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49;
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RA Klausher R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,
RA Klausher R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfelad Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-- SUBCELLULAR LOCATION: Mitochondrial ribosome small subunit
CC (1285) which comprises a 12s rank and about 30 distinct proteins.
CC -- ALTERNATIVE PRODUCTS:

CC -- (1285) which comprises a 12s rank and about 30 distinct proteins.
 Query Match
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[3]
SEQUENCE FROM
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Sasaki H.,
Suzuki H.,
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Hayashizaki Y.;
                                                                                                                                                                                                       EMBL; AB049954; BAB41007.1; -.
EMBL; AK010254; -; NOT_ANNOTATED_CDS.
EMBL; AK010250; -; NOT_ANNOTATED_CDS.
EMBL; BC021752; AAH21752.1; -.
MGD; MGI:1914223; Mrps18b.
GO; GO:0005763; C:mflochondrial small ribosomal subunit;
GO; GO:0003735; F:structural constituent of ribosome; ISS
GO; GO:0006412; P:protein biosynthesis; ISS.
InterPro; IPR001648; Ribosomal_S18.
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PROSITE; PS0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                       mod1f1ed
                                                                                                                                                                                                                                                                                                                                                                                            ils SWISS-PROT entry is copyright. It is produced through a collaboration tween the Swiss Institute of Bioinformatics and the EMBL outstation to European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way diffed and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SINILARITY: BELONGS TO THE S18P FAMILY OF RIBOSOMAL CAUTION: Ref. 2 sequence differs from that shown due frameshift in position 19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId-Q99N84-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409:685-690(2001).
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                                                                                                                                                                   01084; R1bosomal_S18; 1.
PS00057; RIBOSOMAL_S18; FALSE_NEG
                                                                                                                                                   protein;
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Toyo-oka
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                                                                                                                                                     Mitochondrion;
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K., Wang K
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Schoenbach C., Seya T., Shibata Y., Storch K.-I
K., Wang K.H., Weitz C., Whittaker C., Wilming
shida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                     28702
 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      splicing;
                                         X.
                                   MITOCHONDRION (BY SIMILARI 28S RIBOSOMAL PROTEIN S18B Missing (in isoform 2). /FFId=VSP_005723. W; 2284983FD5848791 CRC64;
 Score
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                                                                                                                                                   Transit
 36;
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 B
                                                                                                                                                   peptide;
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Length 254;
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RESULT 12
R18B_HUMAN
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                                                                                                                                                           RX MEDLINE-2238257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang C., Prange C.,

RA Hopkins R.F., Jordan H., Moore G.J., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., WcEwan R.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., KcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Hopkins R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Pituitary tumor;
Zhang Q.H., Guan Z.Q., Dai
Fu G., Luo M., Chen J.H., H
"Human PTD017 gene.";
Submitted (OCT-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R18B_HUMAN STANDARD; PRT; 258 AA.

G9Y676; Q9BS27;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
28 ribosomal protein S18b, mitochondarial precursor
(MIPS18b) (MRP-S18-2) (PTD017 protein) (HSPC183).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-BLOOG;

MEDLINE-20499367; PubMed-11042152;

Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,

Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.,

"Cloning and functional analysis of cDNAs with open reading frames
"Cloning and functional analysis of cDNAs with open reading frames
                     J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-9606;
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Homo sapiens (Human).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 previously undefined genes stem/progenitor cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome
               MEDLINE=21276436; PubMed=11279123;
KOC E.C., Burkhart W., Blackburn K., Moseley A., Spremulli I.
"The.small subunit of the mammalian mitochondrial ribosome:
identification of the full complement of ribosomal proteins
J. Biol. Chem. 276:19363-19374(2001).

J. Biol. Chem. 276:19363-19374(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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out 30 dis
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   ome small distinct
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   subunit
proteins
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RESULT
CP21_HC
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Best Local S
Matches 4
-1- SUBUNIT: CARBOXYPEPTIDASE II IS A DIMER, WHERE EACH MONOMER IS COMPOSED OF TWO CHAINS LINKED BY A DISULFIDE BOND (BY SIMILARIT -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE GERMINATING EMERYO. LOW LEVELS IN THE DEVELOPING ALEURONE AND EMBRYO. ALSO FOUND IN THE ROOTS AND SHOOTS OF THE GROWING SEEDLING.
-1- PTM: THE LINKER PEPTIDE IS ENDOPROTEOLYTICALLY EXCISED DURING ENZYME MATURATION (BY SIMILARITY).
                                                                                                                                                                                   "The expression of serine carboxypeptidases during germination of the barley grain.";
Proc. Natl. Acad. Sci. U.S.A. 91:8209-8213(1994).
-!- CATALYTIC ACTIVITY: preferential release of a or lysine residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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EMBL;
                                                                                                                                                                                                                                                                                               STRAIN=cv. Alexis; TISSUE=Grain; MEDLINE=94336715; PubMed=7520177; Dal Degan F., Rocher A., Cameron-Mills V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare (Barley). Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Serine carboxypeptidase II-1 precursor (EC 3.4.16.6) (CP-MII.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P55747;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HORVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01084; Ribosomal_S18; 1.
PROSITE; PS00057; RIBOSOMAL_S18; FALSE_NEG.
Ribosomal protein; Mitochondrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       999
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:14516; MRPS18B.
GO; GO:0005763; C:mitochondrial small ribosomal subunit;
GO; GO:0003735; F:structural constituent of ribosome; NAS.
GO; GO:0006412; P:protein biosynthesis; NAS.
InterPro; IPRO1648; Ribosomal_S18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Mitochondrial SIMILARITY: BELONGS TO THE S18P FAM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 WYPW 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF100761; AAD43025.1; -. AF151017; AAF36103.1; -. BC005373; AAH05373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 WYPW 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BELONGS TO THE S18P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258
196
29395
                                                                                                                                                                                                                                                                                                                                                                        AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION (BY SIMILARITY).
28S RIBOSOMAL PROTEIN S18B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B4C83E5593796C5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> S (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                  von Wettstein
                                                                                                                                                                                                                                                                            during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poaceae; Pooldeae;
                                                                                                                                                                                                        C-terminal arginine
                                                                                                                                                                                                                                                                               maturation
                                                                                         (BY SIMILARITY).
EMBRYO. LOW
O FOUND IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAS
                                                                                                                                                                                                                                                                                                  D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                               Q8K9J2;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ON_TER
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                           MEDLINE=22084549; PubMed=12089438;
Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S. Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.; "50 million years of genomic stassis in endosymbiotic bacteria."; Science 296:2376-2379 (2002).
-i- FUNCTION: DNA polymerase III is a complex, multichain enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _BUCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00450; serine_carbpept; 1.
PRINTS; PR00724; CRBOXYPTASEC.
ProDom; PD001189; Serine_carbpept; 1.
PROSITE; PS00131; CARBOXYPEPT_SER_HIS;
PROSITE; PS00560; CARBOXYPEPT_SER_HIS;
                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 Buchnera aphidicola (subsp. Schizaphis graminum Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
NON_TER
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOLB_BUCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S10.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
epsilon and theta chains) that associates with a core dimerizes to form the POLIII' complex. PolIII with the gamma complex (composed of gamma, delta, chi chains) and with the beta chain to form the copolymerase III complex (By similarity).
                                                                                                                                        (By similarity). CATALYTIC ACTIVITY:
                                                                                                   + {DNA}(N).
+ {DNA polymerase III contains a core
                                                                                                                                                                       FUNCTION: DNA polymerase III is a complex, multichain responsible for most of the replicative synthesis in k This DNA polymerase also exhibits 3' to 5' exonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 WYPW 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P08819; 1WHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 WYPW 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carboxypeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150
163
41
239
291
109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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162
324
41
239
239
291
121
170
170
170
191
37408
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                                                                                                                                    N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINKER PEPTIDE (BY SIMILARITY).

SERIM CARBOXYPEPTIDASE II-1, C
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                 Schizaphis graminum).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
; 70F081D6B9723A60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SERINE CARBOXYPEPTIDASE II-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ore 36; DB 1;
Pred. No. 71;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zymogen; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                          exonuclease activity
                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 324;
                                                                 PolIII' associates
                                                                                                   (composed of alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
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                                complete
                                                  delta',
                                                                                                                                                                                             in bacteria
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                                , psi and
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RESULT HOUSE AND A COLOR RESULT RESUL
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, 0
01-NOV-1997 (Rel. 35, I
28-FEB-2003 (Rel. 41, I
DNA POLYMETABE III, del
Yano M., Horiuchi T.;

A 718-kb DNA sequence of the Corresponding to the 12.7-28.0 DNA Res. 3:137-155(1996).
                                                                                 MEDLINE-97061202; PubMed-8905232;
Oshima T., Alba H., Baba T., Fujita K.,
Ikemoto K., Inada T., Itoh T., Kajihara
Kimura S., Kitagawa M., Makino K., Masud
Mori H., Motomura K., Nakamura Y., Nashil
Sampei G., Seki Y., Tagami H., Takemoto
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                  Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Science
                                                                                                                                                                                                                                                                                                                              "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                delta and
J. Biol. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene encoding t
III holoenzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carter J.R., Franden M.A., Aebersold R.H., McHenry C.S.; "Identification, isolation, and characterization of the structural gene encoding the delta' subunit of Escherichia coli DNA polymeras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOLB_ECOLI
P28631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93285995; PubMed-8509334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
Enterobacteriaceae; Esche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol.
                                                                                                                                                                                                                                                                                                   complete genome sequence of ice 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z., Onrust R., Skangalis M., O'Don
polymerase III accessory proteins.
a and delta'.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE014110; AAM67896.1;
                                                                                                                                                                                                                                                                                                                                                Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institutions as long and this statement is not removed. s requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WYPW 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268:11758-11765(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8505303;
., Skangalis M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eria; Gammaproteobacteria; Enterobacteriales; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          delta'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38927 MW;
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                                    Escherichia coli K-12 genome
0 min region on the linkage m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160BA0FE21BAD08D CRC64;
                                                                                                                                                                                                                                                                                                                  Escherichia coli K-12.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Donnell M.;
teins. I. holA
                                                                                            A K., Hayashi K., Honjo A.,
Ihara M., Kanai K., Kashimoto K.,
Wasuda S., Miki T., Mizobuchi K.,
Nashimoto H., Nishio Y., Saito N.,
emoto K., Wada C., Yamamoto Y.,
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Guenther B., Onrust R., Sali A., O'Donnell M., Kuriyan J.;
"Crystal structure of the delta' subunit of the clamp-loader
of E. coli DNA polymerase III.";
Cell 91:335-345(1997).
-1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN END
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98028572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY
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                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: DNA polymerase III contains a core (composed of alpha, epsilon and theta chains) that associates with a tau subunit. This core dimerizes to form the POLIII', complex, PolIII', associates with the gamma complex (composed of gamma, delta, delta', psi and chi chains) and with the beta chain to form the complete DNA polymerase III complex. The final composition of the complex is: (alpha, epsilon, theta)[2]-tau[2]-(gamma, delta, delta', psi, chi)[2]-
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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch). This between SWISS-PROT entry is copyright. It is produced through meen the Swiss Institute of Bioinformatics and the Excurpean Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content (See http://www.isb-sib Usage restrictions EMBL Ø for collaboration -L outstation -. Ch outstation n no way

EMBL; L04577; AAA23708.1; -.
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O9wppO chimpanzee
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Q94c39 arabidopsis
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Q51227 neisseria m	Q51227		272	77.1	37	ω
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Q97z77 sulfolobus	Q97277	17	764	79.2	38	7

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RESULT
Q8SVL2
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Q8SVL2 PRELIMINARY; PRT;
Q8SVL2;
01-JUN-2002 (TrEMBLrel. 21, Created)
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Nature 414:450-453(2001).
EMBL; AL590445; CAD26573.1;
InterPro; IPR003151; FAT.
Pfam; PF02259; FAT; 1.
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Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
Katinka M.D., Barbe V., Peyretaillade E., Brottier P., Wincker P.
Prensier G., Barbe V., Peyret P., Saurin W., Gouy M.,
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                                                                                                                                                                                          Pfam; PF00972; Flavi_NS5;
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                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                              "Phylogeny of the genus Flavivirus."; J. Virol. 72:73-83(1998).
                                                                                                                                                                                                                                                                                                                                     MEDLINE-98080391; PubMed-9420202;
Kuno G., Chang G.J., Tsuchiya K.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flavivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 3436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-GB-M1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Encephalitozoon cuniculi.
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                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=64319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yaounde virus
                                                                                                                                                                                                                                                     InterPro;
    Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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IPR007095; RNA_pol_DS_PS.
IPR007094; RNA_pol_PSvir.
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345 A
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(TrEMBLrel.)
(TrEMBLrel.)
(Fragment).
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                                                                                                                                           RDRP_POSITIVE; RDRP_VIRAL; 1.
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39245
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rel. 22, Last
1 ECU05_0540.
                 83.3%;
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Last annotation updat
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Score 40; DB 12;
Pred. No. 1.1e+02;
0; Mismatches 1
                                                                                  DC667CC97761AB5D CRC64;
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                                       Length 345;
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                                                                                                                                                                                                                                                                                                RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA de Pablos M., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P., Burbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Fosler C., Gabrielian A.E., Gargel N.S., Gelbart W.M., Glasser K., RA Fosler C., Gabrielian A.E., Gargel N.S., Gelbart W.M., Glasser K., RA Fosler C., Gabrielian A.E., Gargel N.S., Gelbart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Howland T.J., Wel M.H., Ibeywam C., Jai Z., Kulp D., Lai Z., Kulp D., Lai Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Muzphy B., Muzphy L., Muzny D.M., Nelson D.L., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Martis B., Wolson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Melson D.R., Pettman G.S., Pan S., Pollard J., Puri Y., Reese M.G., RA Malson D.R., Pettman G.S., Pan S., Pollard J., Puri Y., Reese M.G., RA Rahert K., Remington K.A., Saunders R.D., Scheeler F., Smith T., RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., RA Wang Z.Y., Wassarman D.A., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Ra Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., The Genome sequence of Drosophila melanogaster.*;

"The genome sequence of Drosophila melanogaster.*;
         Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., WcIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazedj R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayras-Pfannkoch C., Basley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Beeson K.Y., Botchan M.R., Bouck J., Brokstein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chandra I
                                                                                                                                                             Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8IQJ1;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003
01-MAR-2003
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                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Paragas
ong S., I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophilidae; Drosophila
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Scherer S.E., Li P.W., Hoskins R.A.,
IS S.E., Richards S., Ashburner M., H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=10731132;
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  G.S.,
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  Patel S., Puri V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                              Yang S., Yao Q.A., Ye J.,
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1., Galle R.F.,
Henderson S.N.,
                                                 K.A., Nunoo
                                                                                                                                               Farfan D.,
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RESULT 6
Q9WPP0
ID Q9WPP0
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Best Local S
Matches
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Best Local
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 50.2 kDa protein (Fragment).
Brevibacterium linens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Brevibacteriaceae; Brevibacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-DSM 20426;

MEDLINE-20279196; PubMed-10821176;

Krubasik P., Sandmann G.;

"A carotenogenic gene cluster from lycopene cyclase genes involved in carotenoids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Annotation of Drosophila melanogaster genome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9KK86;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                SEQUENCE
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EMBL; AF139916; AAF65580.1; -.
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Adams M.D., Celniker
Submitted (MAR-2000)
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                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1703;
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EMBL; AE003539;
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Misra S., Crosby M
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5; Conserv
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5; Conserv
                                                                                                                                                                           NGWYPW 6
                                                                                                                             NGWYSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGWYPW 6
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                                                                                                                                                                                                                                                                                                                             456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 AA;
                                                                                                                                                                                                                             Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                           50156 MW;
                                                                                                                                                                                                                                             83.3%;
83.3%;
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e EMBL/GenBank/DDBJ
                                                                                                                                                                                                                        Score 40; DB
Pred. No. 1.4e
0; Mismatches
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PRT;
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the synthesis of aromatic
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1.4e+02;
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investigating biology,";
Science 282:2012-2018(1998).
EMBL; Z80789; CAB02551.1; -.
WormPep; F48C11.2; CE10750.
Interpro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_C; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-FEB-1997 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Q93744;
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprote
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MEDLINE-99370217; PubMed-10438863;
Beer B.E., Bailes E., Goeken R., Dapolito G., Coulibaly C.
Kurth R., Gautier J.P., Gautier-Hion A., Vallet D., Sharp
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beer B.E., Hirsch V.M.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ
EMBL; AF131870; AAD39758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV) Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID=11723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
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01-OCT-2002 (TrEMBLrel.
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Virol. 73:7734-7744(1999).
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Pred. No. 2.8e
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2.8e+02;
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01-DEC-2001
01-MAR-2003
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Malphyhiales; Salicaceae; Populus.

NCBI_TaxID-80863;
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EMBL; AP000984; BAB65951.1; -.
InterPro; IPR001092; HLH_basic.
PROSITE; PS00038; HLH_1; 1.
Transferase; Hypothetical protein; Complete proteome.
SEQUENCE 767 AA; 83742 MW; 277493A13462EC18 CRC66
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                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              PME
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PubMed=11572479;
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                             93E44F3B89E506BA CRC64;
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RP SEQUENCE FROM N.A.

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RR STRAIN-306 / ATCC 13902 / XV 101;

RX MEDIINE-22022145; PubMed-12024217;

RX MEDIINE-22022145; PubMed-12024217;

RA ALVES L.M.C., Go Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite.R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite.R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Machadeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meddanis J., Menck C.F.M., Mayaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Pinlade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Tomparison of the prompes of two Xanthompons nathornes with differing and Comparison of the prompes of two Xanthompons nathornes with differing and Comparison of the prompes of two Xanthompons nathornes with differing and Comparison of the prompes of two Xanthompons nathornes with differing and Comparison of the prompes of two Xanthompons nathornes with differing and Comparison of the prompes of two Xanthompons nathornes with differing and Comparison of the prompes of two Xanthompons nathornes with differing and Comparison of the prompes of two Xanthompons nathornes with differing and Comparison of the prompes of two Xanthompons nathornes and the prompes of two Xanthompons nathornes and the prompes of two Xanthompons nathornes and the prompes of two Xant
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Best Local :
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01-OCT-2002 (
01-OCT-2002 (
01-MAR-2003 (
Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Comparison of the genomes of two host specificities.", Nature 417,459-463 (2002).
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Bacteria; Proteobacteria; Gammaproteobacteria;
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01-MAR-2003
                                                                                   Hypothetical XCC2157.
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PROSITE; PS00178; AA_TRNA_LIGASE_I;
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158 AA; 17
                                                                                                       (TremBirel. 22, Created)
(TremBirel. 22, Last sequence update)
(TremBirel. 23, Last annotation updat)
| protein XCC2157.
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7289 MW; ClB1FB23AA6E930B CRC64;
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ed. No. 68;
Mismatches
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F.F.,
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RX MEDLINE-22022145; PubMed-12024217;
RA da Silva A.C.R. Ferro J.A. Reinach F.C. Farrah C.S., Furlan L.R.,
RA da Silva A.C.R. Ferro J.A. Reinach F.C. Camargo L.E.A.
RA Quaggio R.B. Montediro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Farila J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Klabi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Texeira E.C., Tezza R.I.D.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Texeira E.C., Tezza R.I.D.,
RA Setubal J.C., Kitajima J.P.,
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RA Localities."

RA Martins E.C., Mendonis J.P.,
RT "Experimental S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.,
RT "Experimental S.M., White F.F.,
RA TINdade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA TINDADE SPOINTE; ERNA-Synt_I.
RA Martins E.C., Tezza R.I.D.,
RA Setubal J.C., Kitajima J.P.,
RA "Comparison of the genomes of two Xanthomonas pathogens with differing
RA Lacalities."

RA Hartins E.C., Mendomes Of two Xanthomonas pathogens with differing
RA Hartins E.C., Tezza R.I.D.,
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                                                                                                      Submitted (OCT-2000) to the EMBL/GenBank/DDBJ datemBL; ACO11661; AAF16637.1; ...
InterPro; IPR000070; Pectinesterase.
Pfam; PF01095; Pectinesterase; 1.
PROSITE; PS00503; PECTINESTERASE_2; 1.
SEQUENCE 223 AA; 25031 MW; 289B968B77307882.
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidieurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                          Duesterhoeft A.;
Submitted (FEB-1998) to the EMBL/GenB Submitted (FEB-1998) to the EMBL/GenB EMBL; AL021730; CAAL6831.1; -
GeneDB_SPombe; SPBC4C3.09; -
InterPro; IPR002495; Glyco_trans_8.
Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 376 AA; 44095 MW; 09D82A
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01-JUN-1998 (TrEMBLr
01-JUN-1998 (TrEMBLr
01-MAR-2003 (TrEMBLr
SPBC4C3.09 protein.
SPBC4C3.09.
                                                                                                                         STRAIN-97;
Wood V., I
                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the nitrogen-fixing sympostrizobium loti.";

DNA Rea "Jana"
                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 7:331-338(2000).
EMBL; AP003011; BAB53262.1; -
InterPro; IPR001173; Glyco_trans_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 345 AA; 39450 MW; 131B52D5E56507E1 CRC64;
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                                                                                                                                                                     NCBI_TaxID=4896;
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MEDLINE-21082930; PubMed-11214968;
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01-OCT-2001 (TrEMBLrel. 18,
01-OCT-2001 (TrEMBLrel. 18,
01-MAR-2003 (TrEMBLrel. 23,
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Racteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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     Similarity 4; Conserv
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83.3%;
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 Score 38; DB Pred. No. 2.4e
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K., Kimura T.,
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RESULT 15
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REQUIRE—21927647; pubmed—11930014;

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REDLIRE—21927647; pubmed—11930014;

RESIDENCE FROM N.A.

Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

Ratale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,

Matykh A.G., Koonin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandleri AV19

"The complete genome of hyperthermophile Methanopyrus kandleri AV19

REPLE, REO10353; AAM01820.1; --

GW Complete proteome.

GW Complete Proteome.

GOUENCE 474 AA; 55032 MW; C24446DBB05B5A91 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Query Match 79.2%; Score 38; DB 17; Length 474; Best Local Similarity 80.0%; Pred. No. 3e+02; Matches 4; Conservative 1; Mismatches 0; Indels
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OBTXQ5;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Predicted transposase.
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Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyrus.
Methanopyrus.
NCBI_TaxID=2320;
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179 GWFPW 183
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    ABG90939
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ABG51866
ABB370190
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ABB22333
AAM57746
AAM70159
AAM17988
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Human colon specif
Human colon specif
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Human liver peptid
Peptide #441 enco
Peptide #4525 enco
Protein #4332 enco
Human brain expres
Human bone marrow
Peptide #4422 enco
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3 4	34	34	34	35	35	35	35	35	35	35	35	35	35	35	35	35	<b>3</b> 5	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	36	36	36
	82.9		•							85.4			•			85.4					•	•	•	•	85.4		85.4	•	85.4	•				87.8	
83	61	55	23	1330	974	800	507	507	507	505	505	494	421	379	269	260	260	251	250	248	248	220	209	208	191	189	188	113	109	80	51	20	49	49	49
22	22	22	23	23	23	22	23	18	17	22	19	21	20	20	21	21	21	21	21	24	22	20	22	22	22	21	21	24	22	24	22	23	23	22	22
AAM84712	52	AAU42647	AAU86421	AAU70947	ABP59089	ABB67506	ABB57286	AAW26704	AAR91939	AAG64143	AAW70516	AAY45012	AAY35514	AAY37433	AAY84911	AAG40277	AAG17603	AAG40278	AAG17604	ABP99342	AAU04849	AAY31800	AAU56988	AAU55735	ABG01626	AAG40279	AAG17605	ABU71020	AAO00711	ABU11869	4	710	3979	056	AAM30495
. Human imm	Human imm	Propionibacterium	Androgen	₽	Cell divi	မွ	Ø		Mouse hip			Maize ZmK	Chlamydia	Chlamydia	Amino acid	Arabidops	Arab1dops	Arabidops	Arabidopsis	Orthosomyc	Micromonospora	Beak and	Propionibacterium	0	Novel human	₽	g	_	-		man	be.	n per	tid	Peptide #
immune/haema	1mmune/haema	bacterium	receptor	tuberculosis Rv	lsior	la melanog	haemic c	p7b steroi	hippocampus-	parapsilos	psilo	a	ש	~	d seque	is thal	is thal	is thal	t et	in bi	ospora eve	feather d	pacterium	oacterium			thal	dipocyte Se	-	ecreted pro	tid	losi	tide enc	4308 enc	#4532 enco

# ALIGNMENTS

RESULT 1 ABG90939 ID ABG9 Human; colon specific nucleic acid; CSNA; colon specific polypeptide; CSP; vaccine; diagnosis; metastasis; colon cancer; cancer; immune response; staging; imaging; colorectal cancer; gene therapy; transgenic; engineered colon tissue. ABG90939 standard; Protein; N-PSDB; ABS67078, ABS67079 WPI; 2002-657591/70 Piderit A, Macina RA, 13-FEB-2001; 2001US-268291P 22-AUG-2002. WO200264744-A2 Homo sapiens. Human colon specific polypeptide, #12. 29-NOV-2002 (first entry) ABG90939; (DIAD-) 12-FEB-2002; 2002WO-US04240. DIADEXUS INC. Sun Y, . Liu 51 ₹ ü

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RESULT 2
ABJ04311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention discloses isolated colon specific nucleic acids (CSNAs) and Ct the polypeptides (CSPAs) that they encode. The colon specific nucleic cc acids and polypeptides are useful as vaccines. The colon specific nucleic cc acid and polypeptide are also useful for diagnosing and monitoring the presence and metastases of colon cancer in a patient. The antibody that cspecifically binds to the colon specific polypeptide is useful for CC determining the presence of a colon specific protein in a sample, as well can specific acid molecule or polypeptide. In particularly by inducing an immune cresponse against the colon cancer cell expressing the colon specific concleic acid molecule or polypeptide. In particular, these colon specific cc genes and proteins are useful for identifying, diagnosing, monitoring, cstaging, imaging and treating colon cancer (e.g. colorectal cancer) and cc conor-cancerous disease states in the colon. These are also useful in gene cc therapy, production of transgenic animals and cells and in the production core of engineered colon tissue for treatment and research. The sequences presented in ABG90928-ABG90963 are the human CSPs encoded by the CSNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local :
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                                                           Claim 11; Page 208; 228pp; English.
                                                                                       Novel colon specific polypeptides and polynucleotides useful for detecting, diagnosing, monitoring, treating, staging and predict cancers in humans having cancer and non-cancerous colon disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 178; 187pp; English.
                                                                                                                                                         WPI; 2002-583378/62.
                                                                                                                                                                                                                                                      22-NOV-2000; 2000US-252505P
                                                                                                                                                                                                                                                                                      21-NOV-2001; 2001WO-US43611
                                                                                                                                                                                                                                                                                                                     30-MAY-2002.
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; colon specific gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human colon specific protein SEQ ID NO: 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ04311 standard;
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                                                                                                                                                                                                                       (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                 colorectal cancer;
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43 GGWLPF 48
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5; Conserv
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disease;
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Mismatches
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cytostatic; gene therapy
                                                                                        treating, staging and predicting non-cancerous colon disease
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MG
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The present invention provides protein and coding sequences of human colon specific genes and proteins. These can be used in the treatment of colonic diseases, including colon and colorectal cancers. The present

Query Match
Best Local Similarity
Matches 5; Conser

Conservative

1;

87.8%;

Score 36; DB Pred. No. 19; 1; Mismatches

22;

Length 49

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Indels

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Gaps

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RESULT 3
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                                               liver (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded apptides of the invention.

Note: The sequence information for this patent does not appear in the
                                                                                                                                     The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult
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Sequence
                                                                                                                                                                                                                     Claim
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27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
03-AUG-2000;
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human liver peptide, SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
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                                                                                                                                                                                                                                                                                                           SG,
                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                            genome-derived single exon nucleic acid probes useful sing gene expression in human adult liver -
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                       specification but was obtained in electronic format directly PO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
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5; Conserv
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2000US-0236359.
2000GB-0024263.
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2000US-0632366
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2000US-0207456.
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                                                                                                                                                            The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                      New spatially-addressable set of single exon nucleic acid puseful for measuring gene expression in sample derived from breast, comprises number of single exon nucleic acid probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB31790 standard; Peptide;
                                                                    Sequence
                                                                                          Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                       present sequence is a peptide encoded probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                Claim
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2000US-06323687
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83.3%;
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           Score 36; DB
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1; Mismatches
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           Gaps
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RESULT 5
ABB370
ID ABB3
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ABB370
AC
ABB3
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XX
ABB3
XX
XX
ABB3
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XX
Pept
DE Pept
XX
XX
Huma
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Huma
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O9-A
RESULT 6
ABB22333
ID ABB2
XX
AC ABB2
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26-MAY-2000; 2000US-0208408.
30-JUN-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234589.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn
                           23-JAN-2002
                                                                             АВВ22333;
                                                                                                                                  ABB22333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 29654; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; foetal liver; gene expression; single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04 FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB37019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #4525 encoded by human foetal liver single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG,
                                                                                                                                                                                                                                                                    39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39
                                                                                                                                                                                                                                                                                                                    1 GGWLPY 6
                                                                                                                                  standard;
                                                                                                                                                                                                                                                                    GGWLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGWLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGWLPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                  Protein;
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen
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                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB
Pred. No. 19;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT 7
AAM57746
ID AAM5
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                measuring human gene expression in a sample derived from human heart (see ABA21335-ABA41305). The present sequence is a protein encoded by one sucl probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, stagying, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                        Human; brain expressed exon; gene expression analysis; probe, microarray; Alzheimer's disease; multiple sclerosis; schizopl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene expression; heart; microarray; vascular systemeration cardiocascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
                              epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single exon nucleic acid probes for analyzing
          Homo sapiens
                                                                         Human
                                                                                               05-NOV-2001
                                                                                                                     AAM57746;
                                                                                                                                          AAM57746 standard;
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000;
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27-SEP-2000;
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30-JUN-2000;
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                                                                        brain
                                                                                                                                                                                               39 GGWLPH 44
                                                                                                                                                                                                                    Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                    GGWLPY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID No
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                                                                                                                                                                                                                                                                                    49
                                                                        expressed single
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                          Conservative
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                                                                                              (first entry)
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                                                                                                                                          Protein;
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heart; microarray; vascular system;
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                                                                                                                                                                                                                                          ۲.
                                                                                                                                                                                                                                                   Score 36;
Pred. No.
                                                                        exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for measuring heart cell gene
                                                                                                                                                                                                                                         Mismatches
                                                                        probe encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                   DВ
19;
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                                                                        protein
                                                                                                                                                                                                                                                              Length 49
                                                                                                                                                                                                                                          Indels
                                          schizophrenia;
                                                                        SEQ ID
                                                                                                                                                                                                                                         0;
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Best Local :
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          21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                            which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single
brains
                                                                                                                                                                                   microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                              30-JAN-2001;
                                                                                                                                                                                                                  Human bone marrow expressed
                                                                                                                                                                                                                                          06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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26-MAY-2000;
                                                                                                                     09-AUG-2001
                                                                                                                                          WO200157276-A2
                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                               Human; bone
                                                                                                                                                                                                                                                               AAM70159
                                                                                                                                                                                                                                                                                    AAM70159 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
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27-SEP-2000;
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG,
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                         GGWLPH
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                                                                                                                                                                                                                                                                                                                                                                                                                               49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:
                  ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
                                                                                                                                                                                   marrow expressed exon; gene expression analysis; probe;
cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                               2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                        (first entry)
           2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0180312
2000US-0207456
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                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                           44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DK,
                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                              87.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from genomic sequences expressed in the human to measure gene expression in brain cell samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probes
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                                                                                                                                                                                                                                                                                     49
                                                                                                                                                                                                                    probe encoded protein
                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB Pred. No. 19; 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                             DВ
19;
                                                                                                                                                                                                                                                                                                                                                                                                          22;
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0;

Indels

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Gaps

0;

SEQ ID

NO:

30465

Length 49;

English

in

human

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RESULT 9
AAM17988
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Best Local S
Matches 5
                                                                                                                                                04-FEB-2000;
26-WAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The
The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI20459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used.
                                                                                            WPI;
                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn
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                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                               Peptide
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                                              Claim
                                                               analyzing
                                                                                                                                (MOLE-)
                                                                                                                                                                                                                           30-JAN-2001;
                                                                                                                                                                                                                                                                WO200157278-A2
                                                                                                                                                                                                                                                                                                     cervical cancer.
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                                                                                                                                                                                                                                                                                                                                                                    AAM17988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               marrow. They can be used to market of single les, which market can be used to market of single les, which market of single les, which market of single les.
                                                                                                                                                                                                                                                                                  sapiens.
                                                                                                              SG,
                                                                                            2001-488901/53.
                                              27;
                                                               genome-derived single exon nu
zing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                    39
                                                                                                                                                                                                                                                                                                             human; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which are derived from genomic sequences expressed in the human rrow. They can be used to measure gene expression in bone marrow, which may enable the improved diagnosis and treatment of cancers lymphoma, leukaemia and myeloma. The present sequence is a encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                               #4422
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                                                                                                                                MOLECULAR DYNAMICS INC
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                                              SEQ
                                                                                                             Hanzel
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                                                                                                                                                2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                 entry)
                                              22814;
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                                                                                                             Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30465; 658pp + Sequence Listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 38
                                                                                                                                                                                                                                                                                                                              probe
                                                                                                                                                                                                                                                                                                            gene
                                                                                                             Σ
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                                            487pp;
                                                               exon nucleic acid probes us
n human cervical epithelial
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Pred.
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                                                                                                                                                                                                                                                                                                                               for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid probes useful
                                             English.
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RESULT 10
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                     The present invention relates to single exon nucleic acid prosee AAI31315-AAI57546). The present sequence is a peptide enc such probe. The probes are useful for producing a microarray predicting, measuring and displaying gene expression in sampl from human placenta. The probes are useful for antenatal diag human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     measuring human gene expression in a sample derived epithelial cells. By measuring gene expression, the useful in grading and/or staging of diseases of the
                                                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did no specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cervical cancer.
                                                                                                                                           analyzing
                                                                                                                                                                                                                               04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                            Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2001
                                     Sequence
                                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                                                              WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                   genetic
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zing gene expres
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Similarity
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5; Conser
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2000US-0632366
2000US-0234687
2000US-0236359
2000US-0024263
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2000US-0207456.
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                                     AA;
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                                                                                                                        ID No 30764; 654pp;
                                                                                                                                          erived single expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                            human;
        87.8%;
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83.3%;
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                                                                                                                                         exon nucleic acid
n human placenta -
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Score 36; DB Pred. No. 19; 1; Mismatches
                                                                                                                                                                                          Rank
                                                                                                                                                                                                                                                                                                                                                                                                              for measuring placental gene
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                                                                                                                         English.
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format
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                  Length 49;
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AAM05626
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                                     RESULT 12
                                                                                                                                      Query Match
Best Local
                                                                                                                            Matches
            ABG39797 standard;
                                                                                                                                                                                                  breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly fro at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                             The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by on such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM05626
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                Claim
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03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
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                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     l single exon nucleic acid probe used to measuring gene expression human breast -
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                                                                        GGWLPH 44
                                                                                                  GGWLPY 6
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                                                                                                                                                                                                                                                                                                                                                                            SEQ ID No 14366; 322pp;
                                                                                                                                                                            49
                                                                                                                            Conservative
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2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0207456.
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            Peptide; 49
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                                                                                                                                       87.8%;
83.3%;
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                                                                                                                                      Score 36; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
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                                                                                                                         Mismatches
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    familial idiopathic pulmonary disease; interstitial lung disease; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndropulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                            04-FEB-2000;
26-MAY-2000;
                                                                                                                  (MOLE-')
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                              SG,
                                                                                                                  MOLECULAR DYNAMICS INC
                                                                            Hanzel DK,
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2000US-0632366.
2000US-234687P.
2000US-236359P.
2000US-236359P.
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2000US-207456P
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                                                                            Chen W,
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                                                                              Rank DR;
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Spatially-addressable set of single exon nucleic acid probes, used gene expression in human lung samples

Claim 27; SEQ ID No 29462; 634pp; English.

cc probes; the novel set of probes which hybridise at high stringency to a connected acid expressed in the human lung; measuring gene expression in a cc nucleic acid expressed in the human lung; measuring gene expression in a cc sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of cc the array; identifying exons in a eukaryotic genome, comprising cc (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably clabeled nucleic acids from eukaryote lung mRNA, to a single exon probe, chaving a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method cabove and (b) measuring the expression of each of the exons in several ctissues and/or cell types using hybridisation to a single exon probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising or of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 neurofibromatosis, tuberous sclerosis, particularly O.f

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RESULT 13
AAU71006
ID AAU711
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XX AU711
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Best Local S
Matches 5
The invention relates to a substantially pure polypeptide comprising an amino acid sequence selected from Rv0284, Rv0285, Rv0455c, Rv0455c, Rv19569, Rv19569, Rv1986, Rv3477, Rv3878, Rv3879c or Mr3106.1 (also disclosed are ORF13A and Rv0284ct), or their immunogenic portion, nucleic acids encoding them and an amino acid sequence analogue having at least 70% sequence identity to the polypeptide and is immunogenic. The protein is useful in preparing a pharmaceutical composition for diagnosing tuberculosis and in preparing a vaccine against tuberculosis caused by virulent mycobacteria. The vaccine or immunogenic, pharmaceutical composition can be used prophylactically in a subject not infected with a virulent mycobacterium, or therapeutically in a subject already infected with a virulent mycobacterium. The protein is useful for preventing, treating and detecting infections caused by species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Mycobacterium tuberculosis antigens, useful for diagnosing tuberculosis, and as a vaccine for treating or preventing infections caused by species of tuberculosis complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agger
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3;
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21-FEB-2001; 2001DK-0000283
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersen P,
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                                  cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                 The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating
                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
   treatment of inflammation
                                                                                                                                                                                                                                                                                                                                                        Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytckine; cell proliferation; cell differentiation; vaccine; peptide therapy; stem cell growth factor; haematc tissue growth factor; humanomodulatory, cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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18-MAY-2000; 2000US-0577409
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DB; AAI91177.
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                  leukaemia, nervous system disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cirrhosis; cell proliferative disease; cancer; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; cardiovascular disorder; hypertension; angina pectoris; allergy; myocardial infarction; immune disorder; inflammatory disorder; AIDS; hypothyroidism; acquired immunodeficiency syndrome; Cushing's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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27-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; SECP; secreted protein;
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13-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental disorder.
The invention relates to an isolated polypeptide comprising any of 30 secreted human proteins (SECP1-SECP30) appearing as ABU11846-ABU11875. caturally occurring amino acid sequence at least 90-98 % identical to
                                                                               preventing diseases or cexpression e.g. cancer, hepatitis, cirrhosis -
                                                                                           New human secreted proteins (SECP) useful for diagnosing, treating preventing diseases or conditions associated with the aberrant SECF expression e.g. cancer, AIDS, atherosclerosis, epilepsy, allergies
                                                                                                                                                              WPI;
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                                                      Claim 1; Page 161; 192pp;
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5; Conser
                                                                                                                                                                                    AA, Hafalia AJA, Duggan BM, Warren BA, Emerling BM; ey CM, Arvizu CS, Honchell CD, Nguyen DB, Kallick DR, Au-Young JK, Ramkumar J, Li JX, Thangavelu K, Gietze: Baughn MR, Yao MG, Walia NK, Mason PM, Lal PG, Graman Becha SD, Sapperstein SK, Richardson TW, Tran UK; VS, Tang YT, Azimzai Y, Yan L, Xu Y;
                                                                                                                                                                                                                                                                                 INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GWLPY 39
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2001US-288640P.

2001US-290516P.

2001US-292184P.

2001US-343553P.

2002US-357002P.

2002US-358279P.

2002US-366041P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       2002WO-US12464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.4%; Score 35;
100.0%; Pred. No.
                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   micro-array; liver disease; hepatitis;
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31;
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7 DB,
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RC;
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cc screening for ant/agonists of SECP, generating an expression profile of a sample containing the polynucleotides and an array comprising different containing the polynucleotides and an array comprising different containing the polynucleotides and an array comprising different conjugate the molecules affixed at distinct physical locations on a solid conjugate the continuous nucleotide sequence specifically hybridisable with care the target polynucleotide. The polypeptides and polynucleotides of the target polynucleotide. The polypeptides and polynucleotides are useful in diagnosing, conference of conditions associated with the conference of conference of conference of conditions associated with the conference of conference of conference of conference of conditions associated with the conference of conf
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Sequence 08 AA,

Ş Query Match Best Local Matches 1 GGWLPY 6 Similarity 5; Conserv GNWLPY Conservative 83.3%; Score 35; DB Pred. No. 48; 0; Mismatches 0; Length 80 Indels 0

0

Search completed: August Job time : 15.1928 secs 20, 2003, 12:33:48 Вþ

62

67

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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         and is derived by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1s the number of results predicted by chance to have score greater than or equal to the score of the result being pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB DB
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
      Match
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/Backfiles1.pep:*
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US-09-270-751-4
US-09-168-2188-5
US-09-252-991A-22895
US-09-252-991A-22717
US-09-252-991A-27172
US-09-252-991A-27172
US-09-268-311-3
US-09-185-31-2
US-09-185-31-31-3
US-09-185-31-31-3
US-09-185-31-31-3
US-09-185-31-31-3
US-09-185-31-31-3
US-08-185-31-31-3
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US-08-185-31-31-3
US-08-185-31-31-3
US-08-185-31-3
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US-09-107-532A-5075
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US-09-198-452A-932
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Compugen
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Sequence 8, Appli
Sequence 932, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 18847, A
Sequence 29895, A
Sequence 27211, A
Sequence 27112, A
Sequence 106, App
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Sequence 5075, I
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2, Appli

18, Appli

11, Appli

12, Appli

12, Appli

13, Appli

13, Appli

13, Appli

21, Appli

25, Appli

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6, Appli

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75.6	75.6	75.6	75.6	75.6	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	80.5	80.5	80.5	80.5	80.5
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US-08-460-309-12	TIS-08-152-010A-38	US-08-152-019A-37	US-08-988-856B-25	US-08-752-852A-145	US-09-341-587-3	US-09-326-203A-24	US-09-252-991A-21769	US-09-328-352-5600	US-09-252-991A-18162	US-09-252-991A-27429	US-09-252-991A-23170	US-08-339-582-2	US-08-587-680A-4	US-08-567-375-4	US-08-587-680A-2	US-08-567-375-2	US-08-475-891A-2
Sequence 12, Appl		-	25. A	14	ω				Sequence 18162, A	Sequence 27429, A	Sequence 23170, A		4	Sequence 4, Appli	•	•	Sequence 2, Appli

#### ALIGNMENTS

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RESULT 2
US-09-107-532A-5075
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Best Local Similarity
watches 5; Conserve
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                                                                                                                                                                                                       Sequence 5075, Application US/09107532A
Patent No. 6588275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32682

LENGTH: 497
TYPE: CHETT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32682, Application US/09252991A Patent No. 6551795
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                 NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                      458 GGWIPY 463
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGWLPY 6
                                                                                           STREET: 100 Beaver S
CITY: Waltham
STATE: Massachusetts
                                                       COUNTRY: USA
ZIP: 02354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                               100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.1%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; Pred, No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                     and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                     CORPORATION
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LOCATION: (B) LOCATION 1...104
SEQUENCE DESCRIPTION: SEQ ID NO: 5075:
US-09-107-532A-5075
                                                                                                                           ; TYPE: PRT; ORGANISM: beak and feather disease virus US-09-267-177-8
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Approx No. 6287856
                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
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                                                              Matches
                                                                                         Query Match
                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/267,177
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: 60/077,890
EARLIER FILING DATE: 1998-03-13
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Vaccines against Circovirus Infections FILE REFERENCE: 21099.0057
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ritchie, Branson W. APPLICANT: Niagro, Frank D. APPLICANT: Lukert, Phil D.
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Poet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION
                                                                                                                                                                            ENGTH: 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
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138 GWLPY 142
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                              2 GWLPY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489 REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09267177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
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                                                       85.4%; Pr
100.0%; Pr
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Pred. No.
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                                                                Gaps
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Sequence 4, Application US/08845161A

Patent No. 5976850

GENERAL INFORMATION:
APPLICANT: Lathe, Richard
APPLICANT: Stapleton, Genevieve
APPLICANT: Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED T
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5976850th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вb
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; Sequence 932, Application US/09198452A
; Patent No. 6559294
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Best Local Similarity
"herhes 5; Conserv?
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                                                                                                                                                                                                                              RESULT 6
US-08-845-161A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT ; ORGANISM: Candida parapsilosis US-09-041-075A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ I
SOFTWARE: Pate
SEQ ID NO 8
LENGTH: 505
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LENGTH: 421
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Griffals,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: : Patent No. H002022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/041,075A CURRENT FILING DATE: 1998-03-10
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X-11242 Sequence Lst
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100.0%; Pred. No.
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ches 0;
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2e+02;
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US-09-270-751-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
TYPE: amino acid
TOPOLOGY: linear
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ATTORNEY/AGENT INFORMATION:
NAME: WIISON, MARY J
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
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FILING DATE: 18-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9421093.7
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                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,751
FILING DATE: 17-Apr-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6184350th Glebe Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lathe, Richard
Rose, Kenneth A.
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APPLICATION NUMBER: PCT/GB95/02465 FILING DATE: 18-OCT-1995
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2.4e+02;
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; MOLECULE TYPE: protein;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-270-751-4
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                                                                                                                                 ; ORGANISM: Murine sp. US-09-168-218B-5
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US-09-168-218B-5
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Best Local S
Matches 5
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LENGTH: 507
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PRIOR FILING DATE: 1997-C
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
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                                                                                                                                                                    TYPE: PRT
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                                                             Local Similarity nes 5; Conserv
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REGISTRATION NUMBER: 32,955
REPERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
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49 GWLPY 53
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                                 2 GWLPY 6
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BEST, RUTH
YAU, JOYCE L.W.
                                                                                                                                                                                                                     PatentIn Ver. 2.1
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                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RICHARD F.
                                                                                                                                                                                                                                                   1997-04-04
                                                             85.4%; Score 35; DB 4; Le
100.0%; Pred. No. 2.4e+02;
n. Mismatches 0;
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100.0%; Pred. No. 2.4e+02;
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RESULT 9
US-09-252-991A-18847
US-09-252-991A-18847; Application US/09252991A
; Patent No. 6551795; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

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US-09-252-991A-29895; Sequence 29895, App.; Patent No. 6551795
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US-09-252-991A-29895
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29895
LENGTH: 201
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LENGTH: 140
                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Marc J.
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Best Local S
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                                    FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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CURRENT FILING DATE: 1999-02-18
PRICE APPLICATION NUMBER: US 60/074,788
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NUMBER OF SEQ ID NOS:
NUMBER OF SEQ ID NOS:
EQ ID NO 22211
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                                                                                                                                                                                                                                          quence 22211, Application US/09252991A
tent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 GGWLP 126
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AVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS IVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

NICE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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S: 33142
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JMBER: US 60/074,788
1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.9%;
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Pred. No.
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1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                       US-09-599-360B-106
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SEQ ID NO 27172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27172, Application US/09252991A Patent No. 6551795
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Best Local
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                    Sequence 106, Application US/09599360B Patent No. 6548633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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SEQ ID NO 106
LENGTH: 385
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NAME/KEY: UNSURE
LOCATION: (263)
                                                                                                    PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Marc J.
TITLE OF INVENTION:
TITLE OF INVENTION:
                             NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
                                                                   PRIOR APPLICATION NUMBER: 09/469,099 PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/599,360B CURRENT FILING DATE: 2000-06-21
                                                                                                                                                                                                                            APPLICANT: Bouqueleret, L.

APPLICANT: Jobert, S.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
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                                                                                                                                                                                                                   FILE REFERENCE: GENSET.050CP3
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AVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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100.0%; Pred. No.
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Pred. No.
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hes 0;
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ORGANISM: Homo

Sapiens

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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 426
TYPE: PRT
ORGANISM: HOMO Sapiens
US-09-288-311-3
                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Shi, Yanggu
APPLICANT: Ruben, Steve M.

TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
FILE REFERENCE: PF398P1
CURRENT APPLICATION NUMBER: US/09/268,311
CURRENT TILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: 60/059,133
EARLIER FILING DATE: 1997-09-17
EARLIER APPLICATION UNMBER: 09/154,219
EARLIER APPLICATION NUMBER: 09/154,219
EARLIER RILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 18
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CURRENT FILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: 60/059,133
EARLIER FILING DATE: 1997-09-17
EARLIER APPLICATION NUMBER: 09/154,219
EARLIER FILING DATE: 1998-09-16
ENUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
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US-09-268-311-3
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Best Local Similarity 100.00
"""tches 5; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-268-311-2
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; NAME/KEY: SIGNAL
; LOCATION: -184..-1
US-09-599-360B-106
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Query Match 82.9%; Score 34; DB 4; Le Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09268311
Patent No. 6482923
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Patent No. 6482923
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sh1, Yanggu
APPLICANT: Sh1, Yanggu
APPLICANT: Ruben, Steve M.
TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
FILE REFERENCE: PF398P1
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100.0%; Pred. No. 2.6e+02;
                                      Length 426;
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  Indels
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Gaps
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Db 288 GGWLP 292

Search completed: August 20, 2003, 12:44:23
Job time: 5.1563 secs.
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Match
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Gapop 10.0 , Gapext 0.5
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      DB
   9 US-09-864-761-37631

15 US-10-083-357-859

15 US-10-083-357-997

15 US-10-083-357-997

15 US-10-985-450-32

16 US-10-156-761-13728

16 US-10-278-536-196

17 US-09-742-582-8

18 US-09-742-580-8

19 US-09-742-581-8

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US-09-989-919-85
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Sequence 33, Appl
Sequence 85, Appl
Sequence 859, App
Sequence 907, App
Sequence 934, Appl
Sequence 13728, A
Sequence 13728, A
Sequence 156, Appl
Sequence 8, Appli
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US-09-989-919-85
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SEQ ID NO 85
LENGTH: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Macina, Roberto
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                               OR APPLICATION NUMBER: PCT/USO1/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00665
OR APPLICATION NUMBER: PCT/USO1/00668
OR APPLICATION NUMBER: PCT/USO1/00668
OR APPLICATION NUMBER: PCT/USO1/00668
OR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
                                           FILING DATE:
                                                          APPLICATION NUMBER: PCT/US01/00663
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NUMBER: PCT/US01/00662
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RESULT 5
US-10-083-357-907
; Sequence 907, A)
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                                                                                                                                                                                                                                             SEQ ID NO 859
LENGTH: 55
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Publication No. US20 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/083,357
CURRENT FILING DATE: 2002-02-27
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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D IN ADULT LIVER, SIGNAL
D IN FETAL LIVER, SIGNAL
D IN HETAL LIVER, SIGNAL = 19
D IN HELA, SIGNAL = 21
D IN PLACENTA, SIGNAL = 18
D IN BT474, SIGNAL = 18
D IN BT474, SIGNAL = 16
D IN BTATIN, SIGNAL = 16
D IN BONE MARROW, SIGNAL
D IN BONE MARROW, SIGNAL
N HIT: AW468873.1, EVALUE
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Pred. No.
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TITLE

APPLICANT: Qiandong TITLE OF INVENTION:

Zeng et al. Systemic Discovery of

2 GWLPY 6

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GENERAL INFORMATION:

APPLICANT: Yanofaky, Martin F.

APPLICANT: Pelaz, Soraya

APPLICANT: Ditta, Gary

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants

TITLE OF INVENTION: Exhibiting Modulated Reproductive Development

FILE REFERENCE: 19452A-002400US

CURRENT APPLICATION NUMBER: US/09/853,450

CURRENT FILING DATE: 2001-05-09

NUMBER OF SEO ID NOS: 61

SOFTWARE: Patentin Ver. 2.1

SEO ID NO 32

TEVER. DET
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US-10-083-357-934
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; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-083-357-907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Saccharomyces cerevisiae 
US-10-083-357-934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Qlandong Zeng et al.
TITLE OF INVENTION: Systemic Discovery of New Genes
FILE REFERENCE: 032796-090
CURRENT PFLLICATION NUMBER: US/10/083,357
CURRENT FILING DATE: 2002-02-27
NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 934
                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/09853450 Publication No. US20020194645A1
         Matches
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CURRENT APPLICATION NUMBER: US/10/083,357
CURRENT FILING DATE: 2002-02-27
NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 61
TYPE: PRT
                                                                              OTHER INFORMATION: SEPALLATA3 (SEP3)
                                                                                                    FEATURE:
                                                                                                                   ORGANISM: Arabidopsis thalians
      Local Similarity
nes 5; Conserv
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les 5; Conservative
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5; Conservative
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        Conservative
85.4%; 5--
100.0%; Pr
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100.0%; Pr
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100.0%; Pred. No.
                   Score 35;
Pred. No.
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Pred. No.
      Mismatches
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. 93;
                   DB 10;
2.7e+02;
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93;
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CURRENT APPLICATION NUMBER: US/10/278,536
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 196
LENGTH: 251
TYPE: PRT
ORGANISH: Arabidopsis thaliana
FEATURE:
COTHER INCOMPATION. C145
; OTHER INFORMATION: G145
US-10-278-536-196
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13728
LENGTH: 246
TYPE: PRT
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                        APPLICANT: Broun, Pierre
TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-011
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                   Yu, Guo-Liang
Keddie, James
Ratcliffe, Oliver
Pilgrim, Marsha
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Jiang, Cai-Zhong
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HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                    Adam, Luc
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100.0%; Pred. No. 2.1
vative 0; Mismatches
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. 2.8e+02;
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Gaps

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RESULT 12
US-Q9-742-581-8
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US-09-742-582-8
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; ORGANISM: Candida parapsilosis
US-09-742-582-8
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US-09-742-580-8
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PRIOR FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 505
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Best Local :
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SEQ ID NO 8
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TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
FILE REFERENCE: X-11242 Sequence Lst
Patent No. US20010012615A1
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Best Local Similarity
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APPLICANT: Radding, Jeffrey A
ITTLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
FILE REFERENCE: X-11242 Sequence Lst
CURRENT APPLICATION NUMBER: US/09/742,580
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/041,075
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100.0%; Pred. No.
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2.8e+02;
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RESULT 14
US-10-156-761-12623
US-10-156-761-12623, Application US/10156761
Sequence 12623, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISIIKAWA, JUN
APPLICANT: ISIIKAWA, JUN
APPLICANT: ISIIKAWA, JUN
APPLICANT: ISIIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 5
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9541
LENGTH: 505
TYPE: PRT
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SEQ ID NO 8
LENGTH: 505
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Heidler, Steven A
APPLICANT: Radding, Jeffrey A
TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
FILE REFERENCE: X-11242 Sequence Lst
CURRENT APPLICATION NUMBER: US/09/742,581
CURRENT FILING DATE: 2000-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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nes 5; Conserv
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HORIKAWA, HIROSHI
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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4.9e+02;
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; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO 12623

; LENGTH: 520

; TYPE: PRT

; ORGANISM: Streptomyces avermitilis

US-10-156-761-12623
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Best Local :
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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CURRENT FILING DATE: 2001-05-23
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APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR-
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1
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09-864-761-41798
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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PLICANT: SAKAKI, YOSHIYUKI
PLICANT: HATTORI, MASAHIRA
TLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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COR PILING DATE: 2000-10-04

COR APPLICATION NUMBER: US 60/236,359

COR APPLICATION NUMBER: US 60/236,359

COR PILING DATE: 2001-01-30

COR APPLICATION NUMBER: PCT/US01/00664

COR APPLICATION NUMBER: PCT/US01/00669

COR APPLICATION NUMBER: PCT/US01/00665

COR APPLICATION NUMBER: PCT/US01/00665

COR APPLICATION NUMBER: PCT/US01/00665

COR APPLICATION NUMBER: PCT/US01/00668

COR APPLICATION NUMBER: PCT/US01/00668

COR APPLICATION NUMBER: PCT/US01/00668

COR APPLICATION NUMBER: PCT/US01/00663

COR APPLICATION NUMBER: PCT/US01/00663
                                                  APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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Similarity 83.3%;
5; Conservative
NUMBER: US 60/234,687
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 41798
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Best Local :
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PRIOR FILING DATE: 2000-06-30
PRIOR-APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
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36 GGWIPW 41
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US-09-300-425B-33
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                                     Description
Sequence 33, Appl
Sequence 33, Appl
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41; DB No. 5.2	MOLECULE 338C	MENTS	9-512-082-0 9-791-537-7 9-791-537-7 9-760-469-1 9-760-469-1 9-760-469-1 9-760-469-1 9-760-469-1 9-760-469-1 9-760-469-1 9-760-469-1 9-760-469-1 9-766-3 9-766-4 9-766-4
14; e+06;	ES FOR S		-78364 -112199 -11397 -1397 -1397 -1397 -171560 -33023 -39023 -39034 -14103 -22814 -14103 -22814 -14758 -14
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                                    ; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B; OTHER INFORMATION: antibody clone US-09-512-082-33
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SEQ ID NO 33
LENGTH: 6
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Query Match
                                                                                                                                                                            SEQ ID NO 33
                                                                                                                                                                                                                            TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGLOGENESIS FILE REFERENCE: SCH-1733P2
CURRENT APPLICATION NUMBER: US/09/512,082
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 09/300,425
PRIOR APPLICATION NUMBER: 09/300,425
PRIOR PILING DATE: 1999-04-28
PRIOR PILING DATE: 1999-04-28
PRIOR PILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGIOGENESIS FILE REFERENCE: SCH-1733P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 1999-04-28-
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/300,425B CURRENT FILING DATE: 1999-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NERI, Dario
APPLICANT: TARLI, LOTENZO
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
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                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 34 SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                        ENGTH: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGWLPY 6
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VITI, Francesca
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      100.0%;
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      Score 41;
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      DВ
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RESULT 6
US-10-437-963-112199
; Sequence 112199, Application US/10437963
; GENERAL INFORMATION:
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Best Local Similarity
"hes 5; Conserva
                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-419-128-32682
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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SEQ ID NO 78364
LENGTH: 238
TYPE: PRT
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SEQ ID NO 32682
LENGTH: 497
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Best Local Similarity
Matches 6; Conserv
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/419,128
CURRENT FILING DATE: 2003-04-21
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                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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                                                                                                                  458 GGWIPY 463
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                                                                                                                                                                                           Conservative
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83.3%;
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Pred. No. 9.4e+02;
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                                                                                                                                                                                                                                   Length 497;
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                                                                                                                  US-09-989-919-85
                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapien
PCT-USO2-04240-67
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                                                                                    Sequence 85, Application US/09989919 GENERAL INFORMATION:
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Best Local
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NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin vers
SEQ ID NO 67
LENGTH: 51
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SEQ ID NO 112199
LENGTH: 107
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                                                                        APPLICANT: Macina, Roberto
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CURRENT FILING DATE: 2003-05-14
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/268,291
                                             APPLICANT:
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5; Conserv
Recipon, Herve
Pluta, Jason
Ghosh, Malavika
Sun, Yongming
Liu, Chenghua
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Kovalic, David
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Macina, Roberto
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Pred. No.
                                                                                                                                                                                                                                                 Score 37;
Pred. No.
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2.7e+02;
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3.5e+02;
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                                                                                                                                                                                                                                                             Length 51;
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US-09-760-469-1397, Application US/09760469; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
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Best Local Similarity
Whiches 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prior application data removed -
NUMBER OF SEQ ID NOS: 1983
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1397
LENGTH: 150
                                                        Matches
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CURRENT APPLICATION NUMBER: US/09/989,919
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,505
PRIOR APPLICATION NUMBER: 60/252,505
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 124
                                                                                                                                                                                                                                                     OTHER INFORMATION: )
NAME/KEY: SITE
LOCATION: (115)
OTHER INFORMATION: )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PT254
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OTHER INFORMATION: Xaa
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TYPE: PRT
                                                                                                                                                                    LOCATION: (127)
OTHER INFORMATION:
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                                                                                                                                                                                                            LOCATION: (117)
OTHER INFORMATION:
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                                                                                                                                                                                                NAME/KEY: SITE
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140 GGWLPF 145
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                          1 GGWLPY 6
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                                                     Score 37; DB Pred. No. 6.96
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RESULT 10

US-10-216-583-1397; Sequence 1397, Application US/10216583; GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZ54C1N

and

Antibodies

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                                                                                                                                           US-10-216-583-1397
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                                                                      Matches
                                                                                       Query Match
Best Local
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CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/760,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/214,886 PRIOR FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/179,065 PRIOR FILING DATE: 2000-01-31
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LOCATION: (39)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (92)
OTHER INFORMATION: Xaa
                                                                                                                                                           OTHER INFORMATION: Xaa
                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (148)
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                                                                                                                                                                                                                                LOCATION: (127)
OTHER INFORMATION: Xaa
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                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (115)
THER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                               THER INFORMATION: Xaa equals
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OCATION: (110)
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                                                                    Local Similarity
nes 5; Conserv
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APPLICATION NUMBER: 60/
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140 GGWLPF 145
                                   1 GGWLPY 6
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                                                                      Conservative
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Pred. No.
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_125934C.1.pep
US-10-424-599-171560
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US-10-437-963-104557
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Best Local Similarity
Fighter Strong St
RESULT 13
US-10-219-999-33023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 171560, Application US/10424599 GENERAL INFORMATION:
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SEQ ID NO 171560
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Best Local (
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TITLE OF INVENTION: Soy Nucleic Acid
TITLE OF INVENTION: Plants and Uses
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424
CURRENT FILING DATE: 2003-04-28;
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ORGANISM: Glycine max
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NAME/KEY: unsure
LOCATION: (1)..(175)
OTHER INFORMATION: unsure at all xaa locations
FEATURE:
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ORGANISM: Oryza sativa
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                                                                                                                                169 GGWLPF 174
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Kovalic David K
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Barbazuk, Brad
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Pred. No.
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equence 33023, Application US/10219999 ...

Michael D

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APPLICANT: LIU, JINGONG
APPLICANT: Ste10, JOSHUB
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-31
VENIOR FILING DATE: 2001-08-15
VENIOR FILING 
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US-60-312-544-5701
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Best Local Similarity 83.38
""+ ches 5; Conservative
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; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID MOS: 73128
; SEQ ID NO 39507
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE: 1NFORMATION: Clone ID: 700238067_FLI.pep

US-10-425-114-39507
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US-10-425-114-39507
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GENERAL INFORMATION:
APPLICANT: CAD, YONGWEI
APPLICANT: Edgerton, Michael D
APPLICANT: Hikle, Gregory J.
APPLICANT: KOVALIC, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Zea mays
US-10-219-999-33023
                                                                                                                                                                                        Sequence 5701,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.2%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, M
APPLICANT: Hinkle, Gre
APPLICANT: Kovalic, Dav
                                                                                                                                                                                                                                                                                                                                                     1 GGWLPY 6
||||:
163 GGWLPF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 GGWLPF 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hinkle, Gregory J.
Kovalic, David K.
                                                                                                                                                                              Application US/60312544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 30; Length 382; Pred. No. 1.6e+03;
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Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 382;
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APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)A
CURRENT APPLICATION NUMBER: US/60/312,544
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 10730
SEQ ID NO 5701
LENGTH: 382
TYPE: PRT
ORGANISM: Zea mays
FEATURE: Zea mays
Search completed: August 20, 2003, 13:13:45 Job time: 63.4096 secs
                                                                 В
                                                                                             δÃ
                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: 700238067_FLI US-60-312-544-5701
                                                                                                                                                Query Match
Best Local 9
                                                                                                                               Matches
                                                                                                                                            Local Similarity
                                                               163 GGWLPF 168
                                                                                             1 GGWLPY 6
                                                                                                                           5;
                                                                                                                           Conservative
                                                                                                                                           90.2%;
                                                                                                                      Score 37; DB 31;
Pred. No. 1.6e+03;
1; Mismatches 0
                                                                                                                                                      Length 382;
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GenCore version Copyright (c) 1993 - 2003

5.1.6 Compugen Ltd

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
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1: /cgn2_6/ptodata/1/paa/U
2: /cgn2_6/ptodata/1/paa/U
3: /cgn2_6/ptodata/1/paa/U
4: /cgn2_6/ptodata/1/paa/U
5: /cgn2_6/ptodata/1/paa/U
6: /cgn2_6/ptodata/1/paa/U
7: /cgn2_6/ptodata/1/paa/U
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Match
                       126775 seqs, 26518662 residues
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US00_NEW_COMB.pep:*
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                US-10-294-433-253
US-10-286-897-1865
US-10-286-897-5437
US-10-286-897-5437
US-10-286-897-5437
US-10-286-898A-5437
PCT-US03-19871-10
US-10-401-397A-2
US-10-401-397A-2
US-10-603-114-545
PCT-US03-19871-6
US-10-603-114-545
PCT-US03-19871-2
PCT-US03-19871-2
PCT-US03-19871-6
US-10-603-114-6420
US-10-603-114-6520
US-10-603-113-15574
US-10-603-113-15578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search time 1.73494 Seconds (without alignments) 91.710 Million cell updates/sec
                                                                                                                Sequence 253, App Sequence 1865, Ap Sequence 1865, Ap Sequence 5437, Ap Sequence 10, Appl Sequence 1125, Appl Sequence 1274, Ap Sequence 1274, Appl Sequence 5455, Appl Sequence 5455, Appl Sequence 6420, Appl Sequence 6420, Appl Sequence 6420, Appl Sequence 650, Appl Sequence 550, Appl Sequence 566, Appl Sequence 566, Appl Sequence 566, Appl Sequence 5674, Ap Sequence 5674, Ap Sequence 56574, Ap Sequence 56574, Ap Sequence 56574, Appl 1506
                  Sequence
Sequence
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Sequence
Sequence
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              550, App
550, App
560, App
26574, App
26574, App11
15018, A
7515, App
265, App
4322, Ap
6230, Ap
14700, A
RESULT 2
US-10-286-897-1865
; Sequence 1865, Application US/10286897
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	44444488899999999999999999999999999999	27
	31 32 32 33 31 31 31 31 31 31 31 31 31 31 31 31	32
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	7000000010100010000	o,
ALIGNMENTS	US-10-603-113-15999 US-10-460-614-50 US-10-603-114-782 US-10-603-114-782 US-10-603-114-782 US-10-603-114-783-8159 US-10-612-783-5154 US-10-612-783-5154 US-10-612-783-5155 PCT-US02-41847A-6 US-10-603-114-6379 PCT-US02-41847A-6 US-10-733-573-9338 US-10-739-072-44 US-10-369-072-43	US-10-603-114-4623
•	Sequence 15999, A Sequence 50, Appl Sequence 7525, Ap Sequence 7864, Ap Sequence 26, Appl Sequence 3649, Ap Sequence 3154, Ap Sequence 5155, Ap Sequence 5157, Ap Sequence 6379, Ap Sequence 63, Appl Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl Sequence 42, Appl Sequence 43, Appl Sequence 43, Appl Sequence 256, Appl Sequence 256, Appl Sequence 688, App Sequence 688, App	600

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NUMBER OF SEQ ID NOS: 86/
SOFTWARE: Custom
SEQ ID NO 253
LENGTH: 131
TYPE: PRT
ORGANISM: Homo sapiens
US-10-294-433-253
                                                                                                                                                                                                                                                                                                                                                      CURRENT FILLING DATE: 2002-11-13

PRIOR APPLICATION NUMBER: US/10/294,433

CURRENT FILLING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: 09/989,600

PRIOR FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: 09/577,408

PRIOR APPLICATION NUMBER: 09/577,408

PRIOR APPLICATION NUMBER: 09/577,408

PRIOR FILING DATE: 2000-05-18

PRIOR PILING DATE: 2002-04-02

PRIOR APPLICATION NUMBER: 09/677,298

PRIOR APPLICATION NUMBER: 09/695,781

PRIOR APPLICATION NUMBER: 09/695,781

PRIOR APPLICATION NUMBER: 09/695,781

PRIOR APPLICATION NUMBER: 09/695,781

PRIOR APPLICATION NUMBER: 09/715,802

PRIOR APPLICATION NUMBER: 09/715,802

PRIOR APPLICATION NUMBER: 09/715,809

PRIOR APPLICATION NUMBER: 09/715,809
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US-10-294-433-253
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                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/PRIOR FILING DATE: 2001-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 792CIP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10294433
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Query Match Best Local S Matches

70

GGWLP

1 GGWLP 5 Similarity 5; Conserv

Conservative

82.9%; Score 34; 100.0%; Pred. No. 0;

DB 6; 24;

Length 131; Indels

Mismatches

0;

0

Gaps

CURRENT APPLICATION NUMBER: US/10/286,897

784FLPCT Inc

TLE OF INVENTION: Novel Nucleic Acid and Polypeptides

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US-10-286-897-1865
                                           ; ORGANISM: HOMO: US-10-258-898A-1865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: pt_F
SEQ ID NO 1865
LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/258,898A
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US/99/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/99/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
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Best Local Similarity
Query Match
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PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US/09/620,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/09/653,450 PRIOR FILING DATE: 2000-08-31
                                                                                                                           SOFTWARE: pt_
EQ ID NO 1865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hyseq Inc
                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLE OF INVENTION: Novel Nucleic Acid and Polypeptides
                                                                                                      ENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/727,344 FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-07-19
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                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2000-06-20
APPLICATION NUMBER: US09/620,312
FILING DATE: 2000-07-19
                                                                                                                                                                                                         APPLICATION NUMBER: US09/727,344
                                                                                                                                                                                                                     APPLICATION NUMBER: US09/693,036
FILING DATE: 2000-10-19
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                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US09/653,450 FILING DATE: 2000-08-31
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LING DATE: 2000-10-19
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                                                                                                                                                                                      2000-11-29
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              82.9%;
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              Score
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              34;
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              BB
              6,
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              Length 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: pt_r
; SEQ ID NO 5437
. LENGTH: 310
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Best Local S
Matches 5
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CURRENT FILING DATE: 2002-11-01
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PRIOR APPLICATION NUMBER: US/09/598,042
PRIOR FILING DATE: 2000-06-20
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PRIOR FILING DATE: 2000-01-21
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                                                                                                                                     PRIOR APPLICATION NUMBER: US09/598,042 PRIOR FILING DATE: 2000-06-20
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                                                                              PRIOR APPLICATION NUMBER: US09/653,450
                                                                                                    PRIOR APPLICATION NUMBER: US09/620,312 PRIOR FILING DATE: 2000-07-19
                                                                                                                                                                                                            PRIOR FILING DATE: 2000-01-2
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
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FILING DATE: 2000-09-14
APPLICATION NUMBER: US/09/693,036
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                                               APPLICATION NUMBER: US09/662,191
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Pred. No.
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; ORGANISM: Homo sapiens US-10-408-765A-1125
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PCT-US03-19871-10
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US-10-258-898A-5437
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GENERAL INFORMATION:
APPLICANT: Eli Lilly and Company
TITLE OF INVENTION: Novel Proteins and Their Uses
FILE REFERENCE: X-15815
                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 1125
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SOFTWARE: pt_FL_genes_b Versions 1.0
SEQ ID NO 5437
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APPLICANT: Warrock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
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CURRENT FILING DATE: 2003-07-23
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Taylor, Steven W.
Glenn, Gary M.
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PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1274
LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
US-10-292-798-1274
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CURRENT FILING DATE: 2002-11-13
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                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 10/017,161 PRIOR FILING DATE: 2001-12-18
                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS FILE REFERENCE: 084335/166
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APPLICANT: Abran, Daniel
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US-10-603-114-5455
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; APPLICANT: GARY BRETON
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SEQ ID NO 6
LENGTH: 371
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SEQ ID NO 8
LENGTH: 328
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                                                                                      TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABITITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001
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CURRENT FILING DATE: 2003-07-23
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TITLE OF INVENTION: Novel Proteins and Their Uses
                                                 CURRENT APPLICATION NUMBER: US/CURRENT FILING DATE: 2003-06-2
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CURRENT FILING DATE: 2003-07-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 24
                                  PRIOR APPLICATION NUMBER: US/09/543,681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 24
                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC_FEATURE LOCATION: (1)..(371) OTHER INFORMATION: LP393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
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OTHER INFORMATION: LP394
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NAME/KEY: MISC_FEATURE
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APPLICATION NUMBER: US 60/128,706
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SEQ ID NO 5455
LENGTH: 416
TYPE: PRT
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APPLICANT: Eli Lilly and Company
TITLE OF INVENTION: Novel Proteins and Their Uses
FILE REFERENCE: X-15815
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Best Local
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CURRENT FILING DATE: 2003-07-23
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APPLICANT: YADSULA, DANIEL THEREOF TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF FILE REFERENCE: P1881RIC1P4(US)
CURRENT APPLICATION NUMBER: US/10/617,573
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OTHER INFORMATION: LP391
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Vandlen, Richard
Watanabe, Colin
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                                                                    Williams, P.Mickey
                                                                                                                           Starovasnik, Melissa.
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Grimaldi, J.Christopher
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Godowski, Paul L
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CURRENT APPLICATION NUMBER: PCT/USO3/19871
CURRENT FILING DATE: 2003-07-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 531
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LCCATION: (1)..(531)
OTHER INFORMATION: LP392
PCT-USO3-19871-4
Search completed: August 20, 2003, 12:45:15 Job time: 2.73494 secs
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; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 12
; LENGTH: 502
; TYPE: PRT
ORGANIZM: Homo Sapien
US-10-617-573-12
                                                                                                                                                               Ouery Match 82.9%; Score 34; DB 1; Length 531; Best Local Similarity 100.0%; Pred. No. 94; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Eli Lilly and Company IIILE OF INVENTION: Novel Proteins and Their Uses ILLE REFERENCE: X-15815
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PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/175481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/191007
PRIOR APPLICATION NUMBER: 60/191007
PRIOR FILING DATE: 2000-03-21
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FILING DATE: 1999-04-26
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FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/130232
FILING DATE: 1999-04-21
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## ALIGNMENTS

C;Accession: 139722
R;Hansen, G.; Larribe, M.; Vaubert, D.; Tempe, J.; Biermann, B.J.; Montoya, A.L.; Proc. Natl. Acad. Sci. U.S.A. 88, 7763-7767, 1991
A;Title: Agrobacterium rhizogenes pRiB196 T-DNA: Mapping and DNA sequence of funct A;Reference number: 139720; MUID:91352070; PMID:1909028
A;Accession: 139722 RESULT 139722 ORF12 RESULT D81049 Query Match Best Local Similarity "~+~hes 6; Conserva 밁 Qy A; Note: encoded t disease A; Molecule type: DNA A; Residues: 1-178 < RES> ORF12 - Agrobacterium rhizogenes plasmid pR18196 C;Species: Agrobacterium rhizogenes C;Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 08-Oct-1999 A; Genome: plasmid A; Cross-references: A; Status: preliminary Genetics: 76 GGWLPY 1 GGWLPY within Conservative GB:M60490; 81 σ the T-DNA (transferred 100.0%; NID:g142245; PIDN:AAA22096.1; PID:g142248 0 Score 41; Pred. No. Mismatches w 멂 DNA) segment of the plasmid; ? 0; Length 178 Indels DNA sequence of function 0; Gaps this 0 segme Chi

hypothetical protein NMB1733 [imported] - Neisseria meningitidis (strain MC58 serogro C; Species: Neisseria meningitidis
C; Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001
C; Accession: D81049
R; Tettelin, H; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Elsen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: A81000; MUID:20175755; PMID:10710307 A; Reference number: A81000; A; Accession: D81049

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-167 <TET> A; Cross-references: GB: AE002523; A; Experimental source: serogroup GB:AE002098; NID:g7226980; B, strain MC58 PIDN: AAF42078.1; PID: 9722

NMB1733

Superfamily: Neisseria meningitidis hypothetical protein NMB1733

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RESULT 4
B83012
                             RESULT
S47151
                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein PA5071 [imported] -
C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
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C; Accession: B81828
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outer capsid protein VP2 - African hors C; Species: African horse sickness virus
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A; Residues: 1-235 <S
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A;Reference number: A82950;
A;Accession: B83012
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                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: B83012
R; Stover, C.K.; Pham, X.Q.;
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A; Cross-references: GB: AL162757;
A; Experimental source: serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919 A;Accession: B81828
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Matches 5;
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Best Local :
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i0; MUID:20437337; PMID:10984043
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83.3%;
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83.3%;
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83.3%;
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Pred. No.
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Pred. No.
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                 horse
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S.; Moule, S.;
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                 sickness
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7.2;
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Mungall, K.; Quail, M.A.;
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Rajandream
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K.; Lim,
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submitted to the EMBL Data
submitted to the EMBL Data
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C; Superfamily:
                             A; Experimental source:
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                                            A; Cross-references:
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A; Accession: E90175
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5; Conserv
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hypothetical protein Y32F6A.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #te:
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C; Date: 23-Nov-1994 #sequence_revision 03-Nov-1995 #text_change C; Date: 23-Nov-1994 #sequence_revision 03-Nov-1995 #text_change C; Accession: S47151
R; Vreede, F.T.; Huismans, H. submitted to the EMBL Data Library, September 1993
A; Description: The cloning, characterization and expression of t A; Reference number: S47151
A; Accession: S47151
                                   A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-637 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awa, Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Sulfolobus solfatarious
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change
C;Accession: E90175
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C; Superfamily: African horse sickness virus
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A; Residues: 1-352 <KUR>
A; Cross-references: GB: AE006641;
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A;Residues: 1-1057 <VRE>
A;Cross-references: EMBL:Z26316; NID:g499374;
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EMBL:AL021474;
be: clone Y32F6A
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83.3%;
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83.3%;
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Pred. No.
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Pred.
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                 PIDN:CAA16307.1;
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No.
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35;
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47;
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                      GSPDB:GN00023;
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hi-Ngoc, H.P.; Redder
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                      CESP:Y32F6A.2
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-759 < CO2>
A;Cross-references: EMBL:AF157706; PIDN:AAD49682.1
A;Experimental source: strain 229; variant B
                                                                                                                                                                                                                                                                                                                                  DR1 protein [imported] - human herpesvirus 6 (strain 229)
C;Species: human herpesvirus 6
A;Varlety: strain 229
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C;Accession: T44142; T44239
R;Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett,
J. Virol. 73, 8040-8052, 1999
                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-759 <DOM>
A;CCOSS-references: EMBL:AF157706; PIDN:AAD49614.1
A;Experimental source: strain 229; variant B
A;Genetics: GN1
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A;Variety: strain HST
G;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
G;Accession: T43952; T44059
R;Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawa J. Virol. 73, 8053-8063, 199
A;Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and A;Reference number: Z22732; MUID:99412319; PMID:10482554
A;Accession: T43952
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A;Cross-references: EMBL:AB021506; NID:g4995977; PIDN:BAA78213.1; PID:g4995980
A;Experimental source: strain HST; pop. variant B
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A;Experimental source: strain HST;
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A; Residues: 1-647 <ISE>
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A; Introns: 45/3; 275/3;
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Best Local S
Matches 5
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les 5; Conserv
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1-647 <IS2>
<GN1>
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5; Conserv
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1; Mismatches
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Pred. No.
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                                                                                                                                                      R:Zimmer, W.; Aparicio, C.; Elmerich, C.
Mol. Gen. Genet. 229, 41-51, 1991
Mol. Gen. Genet. 229, 41-51, 1991
A;Title: Relationship between tryptophan biosynthesis and A;Reference number: S17702; MUID:91375449; PMID:1896020
A;Accession: S17702
A;Status: preliminary
                                                                                                                                                                                                                                                    hypothetical protein 1 - Azospirillum brasilense
C;Speckes: Azospirillum brasilense
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: S17702
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A; Map position: 87/1
A; Introns: 87/1
C; Genetics: <GN2:
A; Gene: DR1
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A; Residues: 1-150 <ZIM>
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T52331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Futamura, N.; Mori, H.; Kouchi, H.; Shinohara, K. Plant Cell Physiol. 41, 16-26, 2000 A; Title: Male flower specific expression of genes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Sallx gilgiana
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change
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A; Accession: T52331
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A; Introns: 87/1
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Best Local S
Matches 5
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                            1 GGWLPY 6
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5; Conser
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5; Conserv
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5; Conservative
GGWSPY 45
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                                                         Conservative
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                                                                    85.4%;
83.3%;
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83.3%;
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83.3%;
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                                                                      Score 35;
Pred. No.
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Pred. No.
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Pred. No. 76;
1; Mismatches
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                                                      Mismatches
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33;
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RESULT

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T00656
MADS box pro
N; Alternate
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N;Alternate names: protein F316.19
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 29-Oct-1999
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 29-Oct-1999
C;Accession: T00656
R;Federspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au,
Yysotskaia, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.
submitted to the EMBL Data Library, February 1998
A;Reference number: Z14197
A;Accession: T00656
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A:Gene: ATSP:F316.19; AGL9
A:Gene: ATSP:F316.19; AGL9
A:Map position: 1
A:Introns: 62/2; 90/3; 113/2; 146/3; 160/3; 174/3; 222/2
A:Introns: 62/2; 90/3; 113/2; 146/3; 160/3; 174/3; 222/2
C:Superfamily: transcription factor squa; serum response factor DNA-binding C:Keywords: DNA binding; nucleus; transcription regulation
C:Keywords: DNA binding; nucleus; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>
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A;Molecule type: DNA
A;Residues: 1-251 <FED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MADS box protein D - white mustard
WADS-box protein AGL9 homolog
WADS-box protein AGL9 homolog
C;Species: Sinapis alba (white mustard)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
C;Accession: T10467
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T10467
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bonhomme, F.; Sommer, H.; Bernier, G.; Jacqmard, A. Plant Mol. Biol. 34, 573-582, 1997
A;Title: Characterization of SaMADS D from Sinapis alba A;Reference number: 217032; MUID:97390682; PMID:9247539 A;Accession: T10467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                         probable hydroxylase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C;Accession: T35032
R;Seeger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandr,
                                                                                                                                                                                                                                                                       RESULT 14
T35032
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                                                                  A; Reference number: 221565
A; Accession: T35032
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F; 2-57/Domain:
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C;Superfamily: transcription factor squa; serum response factor DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A; Residues: 1-263 <SEE>
                            A; Molecule
                                                                                                                          submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-254 <BON>
                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
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                            type: DNA
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100.0%; Pr
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Pred. No.
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Search completed: August Job time : 6.19277 secs

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A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987; PMID:9634230 A; Accession: D70875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL079355; PIDN:CAB45588.1; GSPDB:GN00070; SCOEDB:SC4C6.24c A;Experimental source: strain A3(2) C;Genetics:
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                                                                                                                                       C; Geneti
A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                 probable PE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene:
                                                                                                                                                                                                                                                                                                                              R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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                             Q
                                                                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: D70875
                                                                                                                                                                          A; Experimental
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ce: strain H37Rv
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Gapop 10.0 ,
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3 azospirillu
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7 sinapis alb
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AC P26943;
DT 01-AUG-1992 (Rel. 23, Created)
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1 GGWLPY 6 |||:|| 891 GGWIPY 896

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Coat protein SEQUENCE 10

1057 AA;

123063 MW; 95.1%; 83.3%;

2880D3DB091C06C4 CRC64;

DB 1;

Length 1057; Indels

EMBL; U01832; AAA62184.1; -.
EMBL; Z26316; CAA81225.1; -.
PIR; S47151; S47151.
InterPro; IPR001742; Orbi\_VP2.
Pfam; PF00898; Orbi\_VP2; 1.

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800	African horse sickness virus (serotype 3)).	hors	- iö	ickn	ess v	irus	3 (AHSV-3) (African	horse sickness virus
R O O	Viruses; dsRNA viruses; NCBI_TaxID=117204;	3; dsF	172	/iru:	ses;	Reov	Reoviridae; Orbivirus.	
R R R	SEQUENCE FROM N.A. MEDLINE=95088612; PubMed=7996157; Vreede F.T., Huismans H.;	E FRC =9508	FROM N.A. 5088612; T., Huism	.A. 2; Pi Lsmai	M N.A. 8612; PubMed= Huismans H.;	-799	96157;	
집집집	"Cloning, char the major neutronics serotype	eroty	pe :	acter raliza 3.";	izatí ation	ds.	"Cloning, characterization and expression of the gather major neutralization-specific antigen of Africations serotype 3.";	the gene that encodes African horsesickness
488	J. Gen. V -!- FUNCT WHICH	Viro CTION CCH CC	TEST	75:3629- THE VP2 P TITUTE TH	629-3 P2 PR E THE	633 OTE	Gen. Virol. 75:3629-3633(1994). FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTEINS WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID. IT	OTEINS (WITH VP5) ID. IT IS THE
ននន	MAJ	AJOR TARGE IMILARITY:	RGET	BEL	ONGS	TO	MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE. SIMILARITY: BELONGS TO THE REOVIRUSES VP2 FAMILY.	:
88	This SW	ISS-P	ROT	ent	ry is	00	pyright. It is produced	This SWISS-PROT entry is copyright. It is produced through a collaboration
38	the European	European	Bic	info	Bioinformatics	tute	e or Bioinformatics and Institute. There are r	Bioinformatics Institute. There are no restrictions on its
88	use by		rg-	non-profit	ins		institutions as long as its	its content is in no way
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RESULT
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022456; Q8GWQ4;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Developmental protein SEPALLATA3 (Agamous-like MADS box protein AGS SEP3 OR AGL9 OR ATIG24260 OR F3I6.19.

Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid.

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                              Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K. Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar I. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
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16-OCT-2001 (Rel. 40, La
Hypothetical 16.3 kDa pr
Azospirillum brasilense.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Azospirillum.
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Kim C.J., Koo H.L.,
Tangin-Hooper S., L
                                                                                                                                                                                                                                                                                                                                    STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed-11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primordia."
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"The Arabidopsis AGL9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OC cluster.";
Gen. Genet. 229:41-51(1991).
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ky M.F.;
L9 MADS box gene
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           Kwan A.,
J.H., Li
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                                                                                                                                                                                        Dewar K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGL9)
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EMBL; AF015552; *I*EMBL; AC002396; *I*EMBL; AK118696; *I*PIR; T00656; T006

AAB67832.1; AAC00586.1; BAC43290.1;

ALT\_INIT.

T00656; T00656. ; P11746; 1MNM.

InterPro; InterPro;

; T03032; -. ; IPR002487; ; IPR002100;

TF\_Kbox.
TF\_MADSbox

TRANSFAC;

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Lin X., Liu S.X
Militscher J., 1
Pai G., Peterso
Sakano H., Salz
Sun H., Tallon
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complexes of MADS-box proteins are sufficient to convert leaves into floral organs.".

Nature 409:525-529(2001).

Nature 409:525-529(2001).

Hattre 409:525-529(2001).

I development and floral organogenesis. Functions with development and floral organogenesis. Functions with SEPALLATA/AGL2 and SEPALLATA/AGL4 to ensure proper development of petals, stamens and carpels and to prevent the indeterminate growth of the flower meristem. Interacts with APETALAI, AGAMOUS CAPETALAI, AGAMOUS C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theol
"RIKEN Arabidopsis full length cDNA clones
SSP consortium (Salk/Stanford/PGEC).";
Submitted (NOV-2002) to the EMBL/GenBank/DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pelaz 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9418042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          within petals, stamens, and carpels.
MISCELLANEOUS: Triple mutations in the SEP1, SEP2 and SEP3 result in the replacement of the stamens and petals by sepa of the carpels by a new mutant flower with sepaloid organs. Solitarity: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTED 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes regulation during floral meristem development. SUBUNIT: Heterodimer with Apl or AG capable of binding sequences. Binds AP3/PI to form a ternary complex. SUBCELLULAR LOCATION: Nuclear (By similarity). DEVELOPMENTAL STAGE: Expressed early during flower devenithin petals, stamens, and carpels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 K-box dimerization domain.
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i C floral organ
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12:999-1010(1997).
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en the K domains of AG
DNA binding proteins."
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lones (RAFLs) sequenced
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Nierman W.C., Osborne
                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
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RESULT ACCORDED TO THE PROPERTY OF THE PROPERT
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Best Local S
Matches 5
EMBL; Y08626; CAA69916.1; -.

PIR; T10467; T10467.

RISSP; P11746; IMMM.

TRANSFAC; T03170; -.

InterPro; IPR002487; TF_Kbox.

InterPro; IPR002100; TF_MADSbox.

Pfam; PF001486; K-box; 1.

PFAM; PF00319; SRF-TF; 1.

PFAMTS; PR00404; MADSDOMAIN.

SMART; SM00432; MADS; 1.

PROSITE; PS00350; MADS_BOX_1; 1.

PROSITE; PS0066; MADS_BOX_2; 1.

PROSITE; PS0066; MADS_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       between
the Euro
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Sinapis.

NCBI_TaxID-3728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SINAL
                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97390682; PubMed-9247539;
Bonhomme F., Sommer H., Bernier G., Jacqmard A.;
"Characterization of SaMADS D from Sinapis alba sucfunction of the gene: in inflorescence development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Flowering; Transcription regulation; Activ Nuclear protein; DNA-binding; Coiled coil.
DOMAIN 3 57 MADS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agamous-like
AGL9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENT AND FLORAL ORGANOGENESIS.
SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: BELONES TO THE MADS DOMAIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 1 K-box dimerization domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Biol. 34:573-573(1997).
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PF00319; SRF-TF;
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5; Conserv
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(Rel.
(Rel.
e MADS
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94
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Last sequence update)
Last annotation update)
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COILED COIL (POTENTIAL)
; 0057CABD3FlAFC40 CRC6
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Pred. No.
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32;
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ent and floral
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Genew; hu. MIM; 603711; -

HGNC: 2652;

CYP7B1

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RESULT 5
CP7B_HUMAN
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Best Local
   EMBL;
EMBL;
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EMBL;
                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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075881; Q90
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                     limiting) step.
-i- SUBCELLULAR LOCATION: Membrane-bound.
-i- TISSUE SPECIFICITY: Brain, testis, ov.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure and functions of human oxysterc
and gene CYP7B1.";
J. Lipid Res. 40:2195-2203(1999).
-I- PATHWAY: Conversion of cholesterol to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Hippocampus;
MEDLINE-20057832; PubMed-10588945;
Wu Z.L., Martin K.O., Javitt N.B., Chiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the oxysterol disease.";
J. Clin. Invest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver, and Spleen;
MEDLINE-99021668; PubMed=9802883;
MEDLINE-99021668; PubMed=9802883;
Setchell K.D.R., Schwarz M., O'Connell N.C., Lund E.G., Davis D.L.,
Lathe R., Thompson H.R., Tyson W.R., Sokol R.J., Russell D.W.;
"Identification of a new inborn error in bile acid synthesis: mutation
"Identification of a new inborn error in bile acid synthesis: mutation
of the oxysterol 7-alpha-hydroxylase gene causes severe neonatal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome P450 7B1 (Oxysterol 7-alpha-hydroxylase)
                                                                                                                                                                                                                                                                                                                                                                         ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                    Kidney, and small intestine.

kidney, and small intestine.

DISEASE: Defects in CYP7B1 are a cause of neonat hepatitis (MIM:331100). Patients present severe cirrhosis and liver synthetic failure.

SIMILARITY: Belongs to the cytochrome P450 family
AF127090;
AF127090;
AF176805;
AF176800;
AF176801;
AF176802;
AF176803;
AF176803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 GWLPY 249
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 AAC95426.1;
AAD20021.1;
AAK11850.1;
AAK11850.1;
AAK11850.1;
AAK11850.1;
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                     testis, ovary,
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oxysterol 7alpha-hydroxylase
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                                                                                                                                                                                                                                                                                                                                                                     of neonatal
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Matches 5
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q60991;
15-JUL-1999
15-JUL-1999
28-FEB-2003
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                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; FALSE_NEG.
                                                                                                              EMBL; U36993; AAA92615.1; -.
MGD; MGI:104978; Cyp7b1.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1.
                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                             Stapleton G., Steel M., Richardson Morris R.G., Lathe R.;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE-Brain, and Liver; MEDLINE-96102021; PubMed-8530364;
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                            HCT-1.
YP7B1.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Mortia; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CP7B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microsome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Monooxygenase;
                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        "A novel cytochrome P450 expressed primarily in brain.";
J. Biol. Chem. 270:29739-29745(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                    SEQUENCE
                                                                                 PROSITE; PS00086; CYTOCHROME_P450; FALSE_NEG.
Oxidoreductase; Monooxygenase; Electron trans
                                                                                                     PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                              METAL
                                                                       Microsome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0008396; F:oxysterol 7-alpha-hydroxylase activity; TAS GO:0006699; P:bile acid biosynthesis; TAS. erPro; IPR001128; Cytochrome_P450.
                                                                                                                                                                                                                                                                        limiting) step.
SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
subcertuctar tocation: Membrane-bound. Endoplasmic reticulum
mresne specificity: Highly Expressed in Brain; ALSO Express
                                                                                                                                                                                                                                                                                                               PATHWAY: Conversion of cholesterol to
                                                                                                                                                                                                                                                                     LIVER AND KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pro; IPR001128; Cy1
PF00067; P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GWLPY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
5; Conserv
       Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GWLPY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endoplasmic reticulum; Cholesterol metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 (Rel. 38, Created)
9 (Rel. 38, Last sequence update)
3 (Rel. 41, Last annotation updat
p450 7B1 (Oxysterol 7-alpha-hydr
                                                 Endoplasmic reticulum; Cholesterol metabolism.
447 447 IRON (HEME AXIAL LIGAND) (BY
507 AA; 58417 MW; AB3D502F935B7ED6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      506
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         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58255 MW;
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       100.0%; F
tive 0;
                              85.4%;
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R -> H (IN
                  Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07D3D4B801B6DBD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           >>tation update)
7-alpha-hydroxylase) (EC 1.14.13.-)
                                                                                 Electron transport; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cholesterol metabolism.
(HEME AXIAL LIGAND) (BY
                                                                                                                                                                                                                                                                                                                                                       M., Mason
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61;
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61;
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                            Length 507
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VP2_AHSV6
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RRY OCC OC STREET
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Best Local (
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                                                                                                                                                                        LPH_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses;
                                                                                     Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OR L2
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071024;
15-DEC-1998
15-DEC-1998
15-DEC-1998
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Virus Res. 53:53-731198).
                                                                                                                                                                002401; Qbs/14; VV/AC,
01-JUL-1993 (Rel. 26, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lactase-phlorizin hydrolase precursor (Lactase-glycosylceramidase)
Lactase-ractase (EC 3.2.1.108); Phlorizin hydrolase (EC 3.2.1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
SEQUENCE FROM N.A.
STRAIN-Wistar; TISSUE-Intestine;
MEDLINE-91365258; PubMed-1909681;
Duluc I., Boukamel R., Mantei N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTE:
WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID.
MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE.
-i- SIMILARITY: BELONGS TO THE REOVIRUSES VP2 FAMILY.
                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                      Q02401; Q63712;
01-JUL-1993 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coat protein
SEQUENCE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00898; Orbi_VP2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF021235; AAC40994.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98278331; PubMed=9617769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=86060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Outer capsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001742; Orbi_VP2.
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                                                                                                                                             norvegicus (Rat).
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5; Conserv
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(Rel. 37, Last sequence up
(Rel. 37, Last annotation)
protein VP2.
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                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                        063719;
                                                                                                           Rodentia;
                                                                                                                           Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122326 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No.
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                                                                                                         Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2B04DB9E389F4B5F CRC64;
 Semenza
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                                                                                                             Vertebrata;
thi; Muridae;
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   Raul
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                                                                                                             Euteleostomi;
Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
   Freund
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within
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Matches 5
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CONFLICT
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SIGNAL
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CHAIN
DOMAIN
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PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.

PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 2.

PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 2.

Hydrolase; Glycosidase; Zymogen; Signilarit; Transmembrane; Repeat.

Hydrolase; Glycosidase; Zymogen; Signilarity.

BY SIMILARITY.
                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X56748; CAA40070.1; -.
EMBL; X56747; CAA40069.1; -.
EMBL; L04635; AAA41539.1; -.
PIR; JS0610; JS0610.
HSSP; P26205; ICBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The rat LPH gene 5' region: comparative structure with the human gene";
pun Seq. 3:119-121(1992).
-I- FUNCTION: LPH SPLITS LACTOSE IN THE SMALL INTESTINE.
-I- CATALYTIC ACTIVITY: Lactose + H(2)0 = D-glucose + D-galactose.
-I- CATALYTIC ACTIVITY: Glycosyl-N-acylsphingosine + H(2)0 = a sug
                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley;
MEDLINE-93091244; PubMed-1339333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 103:275-276(1991)
[2]
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PRINTS; PR00131; GLHYDRLASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. BRUSH BORDER. TISSUE SPECIFICITY: INTESTINE.

DOMAIN: THE SEQUENCE EXHIBITS 4 REGIONS (I-IV) OF INTERNAL
    1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: THE SEQUENCE EXHIBITS 4 REGIONS (I-IV) OF HOMOLOGY; THEREFORE LPH MIGHT HAVE EVOLVED BY TWO
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                                           N
                                                                                     Similarity
5; Conserv
                           GWLPY 6
GWLPY 1093
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                                                                                                                                 85.48;
                                                                                                                                                                             217266
                                                                                                            100.0%;
                                                                                                                                                                      PROTON DONOR (POTENTIAL):
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (POTENTIAL):
NUCLEOPHILE (BY SIMILARITY).
A -> R (IN REF. 1; AAA41539).
Q -> E (IN REF. 1; AAA41539).
E -> D (IN REF. 1; AAA41539).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of intestinal lactase-phlorizin hydrolase
                                                                                     0
                                                                                                          Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LACTASE-PHLORIZIN HYDROLASE.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BETA-GLUCOSIDASE.
                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rmatics and the EMBL outst
There are no restrictions
ng as its content is in
                                                                                                          2.1e+02;
                                                                                                                          Length 1928
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RESULT 9
NUOE\_RICCN

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RESULT 10
NUHM_ARATH
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Matches 5
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SEQUENCE FROM N.A.
STRAIN-Malish 7;
STRAIN-Malish 7;
MEDLINE-21442074; PubMed-11557893;
MEDLINE-21442074; PubMed-11557893;
MEDLINE-21442074; PubMed-11557893;
MEDLINE-21404074; PubMed-11557893;
MEDLINE-21404074; Pournier P.-E.,
MEDLINE-21404
                       NUHM_ARATH STANDARD; PRT; 244 AA 022769; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat NADH-ubiquinone oxidoreductase 24 kDa subun (EC 1.6.5.3) (EC 1.6.99.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003
28-FEB-2003
15-SEP-2003
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUOE_RICCN
Q92ID9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002023; Cmplx1_24kDa.
Pfam; PF01257; complex1_24kD; 1.
ProDom; PD003859; Cmplx1_24kDa; 1.
PROSITE; PS01099; COMPLEX1_24K; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE008611; AAL03019.1; -. PIR; A97760; A97760.
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-i- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
NADH-quinone oxidoreductase chain E (EC 1.6.99.5) (NADH dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsia conorii.
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96
132
136
167
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19156 MW;
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(Mouse-ear cress).
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
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Pred. No.
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                                                                                      cion update)
kDa subunit,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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                                                                                         mitochondrial precursor
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(POTENTIAL).
(POTENTIAL).
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L outstation -
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RA Massent O., Guigley F., Clabauld G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Cacaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Schon M., Murray J., Sheet P., Cordes M., Aburthreideh J.,
RA Schon M., Murray J., Sheet P., Cordes M., Aburthreideh J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Gerco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Mulson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Mulson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
"Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele De Keyser A., Buysshaert C., Gielen J., Vilarroel R., De Clercq R. Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S., Clark L., Dogett J., Hall S., Kay M., Lennard N., McLay K., Mayes Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H., Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller Auer S., Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A. Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E., Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., Schmidt W., Lecharny A., Aubourg S., Cheffor F., Cooke B., Schmidt W., Lecharny A., Aubourg S., Cheffor F., Cooke B., Berger C., Monfort A., Schmidt W., Lecharny A., Aubourg S.,
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Van der
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-I- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATOR CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BE TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP) FRAGMENT OF THE ENZYME (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor = CATALYTIC ACTIVITY: NAHH + acceptor = NAD(+) + reduced acceptor = NAD(+)
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Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
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Mayer K.F.X., Schueller C., Wambut
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THIS IS A COMPONENT OF THE FLAVOPROTEIN FRACTION.
SUBCELLULAR LOCATION: MATRIX AND CYTOPLASMIC SIDE OF THE
MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
SIMILARITY: BELONGS TO THE COMPLEX I 24 KDA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFACTOR: Binds 1 2Fe-2S cluster (Potential).
SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS
                                                                                                                                                                                                     European
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                                                                                                                                                                                              Bioinformatics Institute.
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(See
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RESULT 11

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"The wheat mitochondrial gene for subunit I of the NADH dehydrogenase complex: a trans-splicing model for this gene-in-pieces.";

Cell 65:465-472(1991).

-i- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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Pfam; PF01257; complex1_24kD; 1.
ProDom; PD003859; Cmplx1_24kDa; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion.
Eukaryota; Viridiplantae;
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15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit metal-binding; Iron-sulfur; Iron; 2Fe-2S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AC002330; AAC78260.1; EMBL; AL161494; CAB80751.1;
                                                                                                                                                                  or send an
                                                                                                                                                                                     entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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NCBI_TaxID=4565;
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HSSP; 066511; 1F37.
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                                                                                                                                                                                                                                               the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY. CAUTION: Positions 1, 72, 103, 146, 164, 167, 179, 191, 19: 225, 245 and 248 are modified by RNA editing.
                                                           ; X57968; CAA41034.1; ; X57967; CAA41034.1; ; X57966; CAA41034.1; ; X57965; CAA41034.1;
                                      A38489; DNWTU1.
                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a lpha sen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                  requires a license agreement an email to license@isb-sib.cl
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RESULT 13
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InterPro; IPRO01594; Resp_NADH_dhl.
Pfam; PF00146; NADHdh; 1.
PROSITE; PS00667; COMPLEX1_ND1_1; 1.
PROSITE; PS00668; COMPLEX1_ND1_2; 1.
                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long or modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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J. Mol. Biol. 250:484-495(1995).
-I- CATALYTIC ACTIVITY: NADH + ui
-I- SIMILARITY: BELONGS TO THE C
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3).
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P48898;
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PROSITE; PS00668; COMPLEX1_ND1_2;
Oxidoreductase; NAD; Ubiquinone; N
RNA editing.
SEQUENCE 325 AA; 35932 MW; BBI
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nilarity 100.0%;
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                                                                                  254
                         STANDARD;
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                                                                                                                                                                          NAD; Ubiquinone; Mitochondrion; AA; 36447 MW; 6D33B81B09173EE2
  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=7616569;
C., Richard O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Florideophyceae; Gigartinales;
                                                                                                                         J.08;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34;
Pred. No.
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Pred. No.
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2; 1.
Witochondrion;
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                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bonnard
                         328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326
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                                                                                                                                     DB 01;
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61;
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                                                                                                                                                    Length 326
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                                                                                                                                                                            CRC64;
                                                                                                                                                                                       Transmembrane
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NUIM_OENBE
ID NUIA_O
AC P31839
DT 01-JUL
DT 15-JUL
DT 15-JUL
DE NADH-U
GN NUD1 OR
OS Oenoth
OG Mitoch
OC EUKARY
OC Sperma
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Best Local S
Matches 5
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01-JUL-1993 (Rel. 2
01-JUL-1993 (Rel. 2
15-JUL-1999 (Rel. 3
SEQUENCE FROM N.A., AND RNA EDITING.

MEDILINE-91208684; PubMed-1850322;

Wissinger B., Schuster W., Brennicke A.;

"Trans splicing in Oenothera mitochondria: nadl mRNA
exon and trans-splicing group II intron sequences.";

cell 65:473-482(1991),

cell 65:473-482(1991),

-I- CAPALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) +

-I- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 F

-I- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eleurosids II; Myrtales; Onagraceae; Oenothera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                     Mitochondrion.
                                                                                                                                                                                                                   Oenothera bertiana (Bertero's evening
                                                                                                                                                                                                                                   ND1 OR NAD1.
                                                                                                                                                                                                                                               NADH-ubiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; NAD; SEQUENCE 328 AA; 3
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                                                                                                                                              NCBI_TaxID=3950;
                                                                                                                                                                                                                                                                                                                       NU1M_OENBE
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PROSITE; PS00667; COMPLEX1_ND1_1;
PROSITE; PS00668; COMPLEX1_ND1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M68929; AAC09438.1; -.
PIR; S25993; S25993.
InterPro; IPR001694; Resp_NADH_dhl.
Pfam; PF00146; NADHdh; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
Marchantiposida; Marchantiidae; Marchantiales; Marchantiineae;
Marchantiaceae; Marchantia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-92114051; PubMed-1731062;
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                                                                                                                                                                                                                                                                                                                                                                                               252
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5; Conserv
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Llarity 100.0%;
Conservative (
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    26, Created)
    26, Last sequence update)
    38, Last annotation update)
    oxidoreductase chain 1 (EC 1.6.5.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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eudicots; Rosidae;
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                             ubiquinol
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RAPARAA
      RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.E.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Bellew R.M., Basu A., Baxeer E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McBerson D.,
RA Meinert K.M., Moy M., Murphy B., Murphy L., Muzpy D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Reminatron K. Sannders R D C. Scheeler F.
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O88A_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9VFN2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00667; COMPLEX1_ND1_1; 1. PROSITE; PS00668; COMPLEX1_ND1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Harappoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative odorant receptor 88a. OR88A OR CG14360.
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InterPro; IPR001694; Resp_NADH_dhl.
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Pred. No.
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TRANSMEM
DOMAIN
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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-!- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT
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CYTOPLASMIC (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).
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                                                     Mismatches
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73;
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MBL outstation –
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Search completed: August Job time: 4.38822 secs 20, 2003, 12:35:01

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DB seq length:
    3666377
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    August 20, 2003, 12:25:21; Search time 11.3494 Seconds (without alignments) 136.423 Million cell updates/sec
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## ALIGNMENTS

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E SEQUENCE FROM N.A.

MEDLINE-91352070; PubMed-1909028;

Hansen G., Larribe M., Vaubert D., Tempe J., Biermann B.J.,

A Montoya A.L., Chilton M.-D., Brevet J.;

"Agrobacterium rhizogenes pRi8196 T-DNA: Mapping and DNA sequence of functions involved in mannopine synthesis and hairy root differentiation.";

Proc. Natl. Acad. Sci. U.S.A. 88:7763-7767(1991).

EMBL; M60490; AAA22096.1; -.

InterPro; IPR006064; Glycosidase.

InterPro; IPR006065; Glycosidase.

InterPro; IPR006065; Glycosidase.

R InterPro; IPR006065; Glycosidase.

R Pfam; PF02027; RolB_RolC; 1.

R Pfam; PF02027; ROLB_ROLC; 1.

R PRINTS; PR00746; GLHYDRLASE41.

SEQUENCE 178 AA; 20069 MW; 22A160EED64C45A8 CRC64;
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01-NOV-1996 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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NCBI_TaxID=359;
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76 GGWLPY 81
                                                                                            6; Conserv
                                               GGWLPY 6
                                                                                     100.0%; Score 41; DB 2; Length 178; llarity 100.0%; Pred. No. 13; Conservative 0; Mismatches 0; Indels
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Neisseria; Proteobacteria; Betaproteobacteria;
                                                                                                                                                                                                                                                                                                                      STRAIN-Z2491 / Serogroup A / Serotype 4A;

MEDLING-2022556; PubMed-10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd

Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Jagels K., Leather S., Moule S., Mingold K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:1809-1815(2000).
EMBL; AE002523; AAF42078.1;
TIGR; NMB1733; -.
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                                                                                                                                                                                         meningitidis Z2491.";
Nature 404:502-506(2000).
EMBL; AL162757; CAB85209.1;
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"Complete DNA sequence of a
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172 AA;
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О9НИВ2;
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrer Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., La Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yu Brody L.L., Coulter S.M., Folger K.R., Kas A., Larbig K., Lin Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004920; AAG08456.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical PA5071.
                                                                                  SEQUENCE FROM N.A. Potgieter A.C., Cloete M., van Dijk Potgieter A.C., Cloete M., van Dijk "A first full outer capsid protein cloning, sequencing, expression and full-length outer capsid VP2-genes c
                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
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TIGRFAMs; TIGR00046; TIGR00046; 2.
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MEDLINE=20437337;
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Bacteria; Proteobacteria;
Pseudomonadaceae; Pseudomo
                                         virus serotypes.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ
EMBL; AY163330; AAN74570.1; -
SEQUENCE 1057 AA; 123656 MW; 43EF1F41E37EE
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WEDLINE-21332296; PubMed-11427726;

A She Q. Singh R.K. Confalonieri F., Zivanovic Y., Allard G.,

A Awayez M.J. Chan-Weiher C.C.-Y. Clausen I.G., Curtis B.A.,

A De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

A Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

A Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Charlebois R.L., Bensen C.W., Van der Oost J.;

The complete genome of the crenarchaeon Sulfolobus solfataricus p2."

PROC. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

REMBL; AED066657; ARA40660.1;

REMBL; AED06667; ARA40660.1;
Salanoubat M., Genin S., Arriguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moissan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
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Bacteria; Proteobacteria; Betaproteo
Ralstoniaceae; Ralstonia.
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Sulfolobus solfatar
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STRAIN-U1102;
MEDILINE-91374590; PubMed-1654446;
Martin M.E., Nicholas J., Thomson B.J.
"Identification of a transactivating
                                                              Nature
[6]
                                                                     MEDLINE=91226542; PubMed=1851252;
Thomson B.J., Efstathiou S., Honess R.W.;
"Acquisition of the human adeno-associated human herpesvirus type-6.";
Nature 351:78-80(1991).
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Teo I.A., Griffin B.E., Jones M.D.;
"Characterization of the DNA polymerase
J. Virol. 65:4670-4680(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95266321; PubMed=7747482; Gompels U.A., Nicholas J., Lawren Martin M.E., Efstathiou S., Craxt "The DNA sequence of human herpes and genome evolution.";
                                                                                                                                                                                                                                                                                                          "Human herpesvirus 6 is closely related J. Virol. 64:287-299(1990).
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Viruses; dsDNA viruses,
Betaherpesvirinae; Roseo
NCBI_TaxID=10368;
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Efstathiou S., Craxton M., Macaulay H.A.,
ace of human herpesvirus-6: structure, c
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Efstathiou S., Lawrence G.L., Brow "Identification of homologues to t family in human herpesvirus 6."; J. Gen. Virol. 73:1661-1671(1992).
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J. Virol. 66:3918-3924(1992).
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MEDLINE=94025558;
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Liu D.X., Gompels U.A., Nicholas J.,
"Identification and expression of the
H and interaction with an accessory.
                                                                                                                                                  MEDLINE-93224882; PubMed-8385692;
Sompels U.A., Carrigan D.R., Carss A.
"Two groups of human herpesvirus 6 id
laboratory strains and variants from
                  STRAIN-U1102
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Virology
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Dewhurst S., Dollard S.C., Pellett P.E.,
"Identification of a lytic-phase origin
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Nicholas J.;
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                               Thompson
Frenkel N
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Schiewe U., Neipel F., Schreiner
"Structure and transcription of a
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J. Virol. 67:7680-7683(1993).
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herpesvirus 6 and relationship to rep
J. Gen. Viról. 76:451-458(1995).
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J. Virol. 68:2978-2985(1994).
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                                 Rosenthal
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    Isegawa Y., Mukai T., Nakano K., Kagawa M., Ch. Sunagawa T., Sashihara J., Zou P., Kosuge H., 'A comparison of the complete DNA sequences be to variant A and B.", J. Virol. 0:0-0(1999).

EMBL; AB021506; BAA78213.1; -.

InterPro; IPR002965; P_rich_extensn.

InterPro; IPR003360; US22.
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PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
SEQUENCE 637 AA; 72425 MW; 9C31788B8C04E013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology.";
Science 282:2012-2018(1998).
EMBL; ALO21474; CAA16307.1; -.
WormPep; Y32F6A.2; CE16609.
InterPro; IPR000175; Na/ntran_symport.
Pfam; PF00209; SNE; 1.
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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01-JUN-1998 (TremBLrel.
01-MAR-2003 (TremBLrel.
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MEDLINE-99069613; PubMed-9851916;
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83.3%;
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DT 01-MAX*
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Best Local
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01-MAY-2000
01-OCT-2002
                                                                                                       STRAIN-229;
MEDLING-99412318; PubMed-10482553;
Dominguez G., Dambaugh T.R., Stame
SEQUENCE FROM N.A.
                                    "Human herpesvirus 6B genome with human herpesvirus 6A.";
J. Virol. 73:8040-8052(1999).
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Banuelos M.A., Garciadeblas B.,
"Inventory of HAK transporters ;
submitted (JAN-2002) to the EMBI
EMBL; AJ427975; CAD20996.1;
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   Betaherpesvirinae;
NCBI_TaxID=32604;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID-4530;
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Pfam; PF02705; K_trans; 1.
TIGRFAMs; TIGR00794; kup; 1.
SEQUENCE 715 AA; 79662 MW; B708C
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PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 647 AA; 69466 MW;
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Q8XQH8;
Q1-MAR-2002 (TrEMBLrel. 20, Create)
Q1-MAR-2002 (TrEMBLrel. 21, Last a)
Q1-JUN-2002 (TrEMBLrel. 21, Last a)
Probable transcription regulator p)
RSP1247 OR RS03191.
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Pellett P.E., Dominguez G., Dambaugh T.R., Stamey F.R.,
Inoue N.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF157706; AAD49682.1;
EMBL; AF157706; AAD49681.1;
EMBL; AF157706; AAD49681.1;
InterPro; IPR002955; P_rich_extensn.
InterPro; IPR003360; US22.
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Q94DV0;
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Bukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2001) to the EMBL; AP003255; BAB62587.1; Gramene; Q94DY0; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-cv. Nipponbare;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone: P0454H12.
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                                                                                                                                                              Plasmid megaplasmid.
Bacteria; Proteobacteria;
Ralstoniaceae; Ralstonia.
   STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                  NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
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5; Conserv
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A; 82564 MW;
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83.3%;
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Last sequence update)
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Pred. No. 2.8e+02;
1; Mismatches 0
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Pred. No.
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a; Poales; Poaceae;
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Search completed: August 20, Job time : 14.4605 secs
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Best Local S
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Best Local
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Nature 415:497-502(2002).
EMBL; AL646083; CAD18398.1; -.
InterPro; IPR000005; HTHARAC.
Pfam; PF00165; HTH_ARAC.
PARINTS; PR00032; HTH_ARAC. 1.
SMART; SM00342; HTH_ARAC. FAMILY_1; 1.
PROSITE; PS00041; HTH_ARAC.FAMILY_2; 1.
PROSITE; PS01124; HTH_ARAC.FAMILY_2; 1.
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Siguier P., Thebault P., W
Weissenbach J., Boucher C.
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Arlat M., Billault A., B.
Chandler M., Choisne N.,
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Raymond C.K., Sims E.H., Kas A., Spencer D.H., Kutyavin T.V., Ivey R.G., Zhou Y., Kaul R., Clendenning J.B., Olson M.V.; "Qenetic Variation at the O-Antigen Biosynthetic Locus in Pseu aeruginosa.";
J. Bacteriol. 184:3614-3622(2002).
EMBL; AF498403; AAM27596.1; -.
SEQUENCE 382 AA; 43581 MW; 565B3B2F274764D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Les 5; Conserv
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                                                                                                                                                                                                        Similarity 83. 5; Conservative
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83.3%;
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83.3%;
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Brottler P., Camus J.C., Cattolico L.,
Claudel-Renard C., Cunnac S., Demange N.,
Joisan A., Robert C., Saurin W., Schiex T.,
Whalen M., Wincker P., Levy M.,
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                               2003, 12:40:35
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Last sequence update)
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Pred. No. 1.7e
1; Mismatches
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Pred. No.
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1.7e+02;
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AAY53774
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Human secreted pro
Pinus radiata cell
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VL component of an
Human scFV L19 ant
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## ALIGNMENTS

RESULT 1 AAY56833 WPI; Cervone F, 08-JUN-1998; 08-JUN-1999; (AGRA-) IST AGRARIO DI SAN MICHELE ALL'ADIGE. W09964600-A1 Malus domesticus. Apple LRPKm1 LRR sequence #8 11-APR-2000 AAY56833; AAY56833 standard; peptide; 24 16-DEC-1999. LRPKml gene; leucine-rich protein kinase; apple; fungal pathogen; Venturia inaequalis; transgenic plant; plant defense; scab; LRR. 2000-147095/13 De Lorenzo (first entry) 98IT-RM00367. 99WO-IT00165 ر. ق Komjanc A X

New leucine-rich protein useful to increase plant resistance to fungal pathogens, especially Venturia inaequalis  ${\color{black} \cdot}$ 

Disclosure;

Fig

4.

45pp;

English

kinase

from

apple

es to a LRPKml gene encoding a leucine-rich protein (Malus x domestica) cultivar Florina responsible fo fungal pathogen Venturia inaequalis. Vectors

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resistance to the fungal pathogen Venturia inaequalis. Vectors comprising the polynucleotides can be used to produce transgenic plants (especially apple species; resistant to fungal pathogens, especially V. inaequalis. For example, the gene sequence encoding the protein could be incorporated with the 3Ss promoter of the CaMV cauliflower mosaic virus to introduce a plant defense mechanism against the pathogen, or the promoter sequence upstream from the gene could be used in chimeric constructs to promote sequences encoding for proteins which inhibit V. inaequalis. V. inaequalis is the most severe and economically important fungal pathogen of apples, causing a disease known as scab. Sequences AAY56826-848 represent apple LRPKml LRR sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             age-related macular degeneration; tumour; immunoscintigraphic o
blood coagulation; blood vessel occlusion; ocular anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY53774;
                          The present sequence represents the VL component of a modified human scFv antibody which has specific affinity for a characteristic epitope of the ED-B domain of fibronectin. The affinity of the antibody for this epitope was improved by introducing a number of mutations in the complementarity determining region (CDR) residues located at the
                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scFv; antibody; ED-B domain epitope; ribronectin, images, antibody; ED-B domain epitope; ribronectin, amazor, angiogenesis; vascular proliferation; diabetic retinopathy; angiogenesis; vascular proliferation; tumour; immunoscintigraphic detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VL component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY53774 standard;
                                                                                                                                                                                                                                                                                                                                                                           WO9958570-A2
              complementarity determining region periphery of the binding site. The
                                                                                                                 Claim 10;
                                                                                                                                             antibodies
                                                                                                                                                            Fibronectin
                                                                                                                                                                                                                  Neri D,
                                                                                                                                                                                                                                              (EIDG-)
                                                                                                                                                                                                                                                                         28-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGRIPP 6
                                                                                                                                                                                                                   Tarli L,
  markers
                                                                                                               Page 38;
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                                                                                                                                                          ED-B domain
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99US-0300425.
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  of angiogenesis,
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                                                                                                               59pp;
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                                                                                                                                                          epitope specific antibodies
                                                                                                                 English.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 improved specificity for fibronectin.
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No.
    improved antibody is used for rapid
for detecting diseases characterized
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RESULT 3
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Best Local S
Matches
                 rne invention relates to an antibody with specific affinity for a characteristic epitope of the ED-B domain of fibronectin, where the antibody has improved affinity to ED-B. The invention also relates to conjugates comprising antibodies with a suitable photoactive molecule useful in the detection and/or coagulation of blood vessels. An antibody with improved affinity to the ED-B domain is useful for diagnosis and therapy of tumours and diseases characterised by vascular proliferation, cancer, rheumatoid arthitis, neo-vasculature associated ocular disorders and psoriasis. Treatment of anglogenesis related pathologies comprises the injection of conjugates comprising antibody and a molecule capable of inducing blood coagulation and blood vessel occlusion. The present sequence is single-chain variable antibody fragment (scrv) in antibody variable limbs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by vascular proliferation, such as diabetic retinopathy, age-related macular degeneration or tumours. The antibody localizes the respective tissue within 3 to 4 hours after injection. It is used in immunoscintigraphic detection of angiogenesis and for diagnosis and therapy of tumours and diseases characterized by vascular proliferation. The antibody can be conjugated to a molecule which induces blood coagulation and blood vessel occlusion. These conjugates are used in the preparation of injectable compositions for the treatment of angiogenesis-related pathologies, especially caused by or associated with ocular angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ScFv; single-chain variable antibody fragment; cancer; cytotox coagulant; ED-B domain; fibronectin; tumuor; coular disorder; psorias vascular proliferation; rheumatoid arthritis; blood vessel occlusion; anglogenesis; blood coagulation; variable light chain; VL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                             An antibody, with specific affinity for ED-B domain of fibronectin for the treat by vascular proliferation –
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenesis;
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                                                                                                                                                                                                                                                 Claim 10;
                                                                                                                                                                                                                                                                                                                                                WPI; 2001-541701/60
                                                                                                                                                                                                                                                                                                                                                                                                               (EIDG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2000; 2000US-0512082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-FEB-2001; 2001WO-EP02062
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                                                                                                                                                                                                                                                                                                                                                                                                               EIDGENOESSISCHE TECH HOCHSCHULE
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                                                                                                                                                                                                                                                Page 36; 73pp; English
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Pred. No.
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                                                                                                                                                                                                                                                                                                     treatment
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                                                                                                                                                                                                                                                                                                     a characteristic tment of diseases
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psoriasis;
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RESULT 4
AAB25366
ID AAB25366
ID AAB25366
ID AAB25366
AC AAB2
XX AAB2
AX AAB2
AX AAB2
AX AAB2
AX AAB2
AX AAB2
AX BECCO
KW ELCO
KW ENV
OS Pin
XX PIN
XX PIN
PR 11-:
PR 11-:
PR 01-1
XX ISO
PR 18191
PT 150
PT 180:
PT 150
PT 180:
PT 150
PT 160
CC AAAA
CC AAAA
CC AAAA
CC Bard
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Grandes 6; Conserve
                                                                                                                                                             AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide CC and protein sequences isolated from eucalyptus (Eucalyptus grandis) or CC pine (Pinus radiata also known as Monterey pine). The protein sequences CC are involved in cell signalling. The polynucleotide and protein cCC sequences can be used to modify the response of plant cells to external CC signals e.g. environmental changes or pathogens during the growth and CC development of a plant. They can be used to modify cell proliferation, CC differentiation, elongation and survival, resistance to disease and CC nutrient metabolism. Examples of modifications which can be produced are CC altered fruit ripening and senescence of leaves and flowers e.g. to CC delay senescence and prolong the life of cut flowers or enhance CC modifications can be used to delay senescence in selected cell types or CC croans providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in CC crost tree species giving long stretches of valuable knot-free clear covered to the can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified r to external signals - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signalling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strabala TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2000; 2000WO-US00724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pinus radiata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pinus radiata cell signalling involved protein SEQ ID NO:685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB25366 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 TGRIPP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 314; 527pp;
                100.
nilarity 100.
Conservative
                                                                                                                                 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0228986
99US-0162866
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100.0%; Pr
                0.0%;
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                                          Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽
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                                       DB
47;
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47;
                                                                   21;
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                                                                Length 109;
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 108;
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              0;
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           Gaps
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           0;
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RESULT 5
AAGOO142
ID AAGO
XX AAGO
XX AAGO
XX Huma
XX Huma
XX Huma
XX Homo
PN EP10
XX 20-5
PN 20-5
PN 21-F
PR 26-F
XX Clai
XX PT diag
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RESULT 6
AAB25115
ID AAB2
XX
AC AAB2
XX
DT 27-N
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                     AAB25115;
                                                                                                     AAB25115 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
                                                                                                                                                                                                                                          136 TGRIPP 141
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                                                                                                                                                                                                                                                                                            1 TGRIPP 6
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                                                                                                                                                                                                                                                                                                                                               Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC00148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 AA;
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:
                                                                                                        153
                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                         Score 34;
Pred. No.
                                                                                                     A
                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      62;
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                                                                                                                                                                                                                                                                                                                                                                                            21;
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                                                                                                                                                                                                                                                                                                                                                                                            Length 144;
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27 - NOV - 2000

(first entry)

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RESULT 7
AAB25326
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                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signalling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotide encoding a polypeptide involved in celsignaling used for generating transgenic plants with modified to external signals \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strabala TJ,
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01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-) GENESIS RES & DEV CORP
             Eucalyptus grandis; Pinus radiata;
plant cell signalling; modulation;
environmental change;
                                                          Eucalyptus
                                                                                      27-NOV-2000
                                                                                                                                             AAB25326
                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                   126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Page 82-83;
                                                                                                                                                                                                                                                1 TGRIPP 6
                                                                                                                                                                                                                                                                         6;
                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                   TGRIPP 131
                                                                                                                                               standard;
                                                          grandis cell signalling
                                                                                                                                                                                                                                                                                                                                  153
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US00724.
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99US-0162866
                                                                                                                                                                                                                                                                                                                                  AA;
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                                                                                                                                             Protein;
                                                                                      entry)
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                                                                                                                                                                                                                                                                                       100.0%;
  development;
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                                                                                                                                                                                                                                                                                       Score 34;
Pred. No.
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                                                                                                                                                                                                                                                                            red. No. 66;
Mismatches
 Monterey pine; plant; modification; transgenic plant; pathogen; growth; cell proliferation; differentiation
                                                           involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                             protein
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                                                                                                                                                                                                                                                                                                      Length 153;
                                                                                                                                                                                                                                                                            Indels
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                                                              SEQ
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                                                              ID NO:645
                                                                                                                                                                                                                                                                            0;
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RESULT 8
AAB25447
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and protein sequences isolated from eucalyptus (Bucalyptus grandis) or pine (Pinus radiata also known as Monterey Pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and cavelopment of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to caltered fruit ripening and senescence of cut flowers or enhance senescence of reproductive organs to engineer sterile plants. Other conceptions can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot-free clear wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified to external signals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elongation; survival; disease resistance; nutrient metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strabala TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200042171-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
                                                                             Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modifi plant cell signalling; modulation; transgenic plant; pathogen; environmental change; development; cell proliferation; differen elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                                                              Pinus radiata
                                                                                                                                                                                             27-NOV-2000
                                                                                                                                                                                                                                                          AAB25447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                             AAB25447;
                WO200042171-A1
                                                                                                                                                                                                                                                                                                                                           116 TGRIPP 121
                                                                                                                                                                                                                                                                                                                                                                        1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 294;
                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US00724
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nieuwenhuizen NJ
                                                                                                                                                                cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0228986
99US-0162866
                                                                                                                                                             signalling involved protein SEQ ID NO:766
                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                        ored. No. 66;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified responses
                                                                                                   differentiation
                                                                                                                                                                                                                                                                                                                                                                                                               0
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PR PF F F PR XXX
                                                                                                                                                                                                                                                                                                                                 RESULT 9
AAB25432
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                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and protein sequences isolated from eucalyptus (Eucalyptus grandis) or C pine (Pinus radiata also known as Monterey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein consense can be used to modify the response of plant cells to external C signals e.g. environmental changes or pathogens during the growth and C development of a plant. They can be used to modify cell proliferation, C intrient metabolism. Examples of modifications which can be produced are C altered fruit ripening and senescence of leaves and flowers e.g. to C elay senescence and prolong the life of cut flowers or enhance C modifications can be used to delay senescence in selected cell types or corgans providing fruit and vegetables which have a longer shelf life corest tree species giving long stretches of valuable knot-free clear c wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 6
12-JAN-1999;
01-NOV-1999;
                                                                                                                                                       Eucalyptus grandis; Pinus radiata; plant cell signalling; modulation; environmental change; development; elongation; survival; disease resignation;
                                      11-JAN-2000; 2000WO-US00724
                                                                      20-JUL-2000.
                                                                                                                             Pinus radiata.
                                                                                                 WO200042171-A1
                                                                                                                                                                                                                       Pinus radiata cell signalling involved protein SEQ
                                                                                                                                                                                                                                                            27-NOV-2000
                                                                                                                                                                                                                                                                                                                AAB25432 standard; Protein; 224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-476052/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                          126 TGRIPP 131
                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 355; 527pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000WO-US00724.
990S-0228986
990S-0162866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nieuwenhuizen NJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0228986.
99US-0162866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB
Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                             Monterey pine; plant; modification; transgenic plant; pathogen; growth; cell proliferation; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                          ID NO:751
                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 10
AAY53775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and protein sequences isolated from eucalyptus (Eucalyptus grandis) or CC pine (Pinus radiata also known as Monterey pine). The protein sequences CC are involved in cell signalling. The polynucleotide and protein CC sequences can be used to modify the response of plant cells to external CC signals e.g. environmental changes or pathogens during the growth and CC development of a plant. They can be used to modify cell proliferation, CC differentiation, elongation and survival, resistance to disease and CC nutrient metabolism. Examples of modifications which can be produced are CC altered fruit ripening and senescence of leaves and flowers e.g. to CC delay senescence and prolong the life of cut flowers or enhance CC modifications can be used to delay senescence in selected cell types or cryans providing fruit and vegetables which have a longer shelf life CC between harvest and consumption, or to decrease branching frequency in CC crost tree species giving long stretches of valuable knot-free clear cc wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
   Neri D,
                         (EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH.
                                                       11-MAY-1998;
28-APR-1999;
                                                                                                  11-MAY-1999;
                                                                                                                              18-NOV-1999
                                                                                                                                                                                                                                        angiogenesis; vascular proliferation; diabetic retinopathy; age-related macular degeneration; tumour; immunoscintigraphic detection; blood coagulation; blood vessel occlusion; ocular angiogenesis.
                                                                                                                                                                                                                                                                              scFv; antibody; ED-B domain epitope; fibronectin;
                                                                                                                                                                                                                                                                                                       An antibody with improved specificity for fibronectin.
                                                                                                                                                      WO9958570-A2
                                                                                                                                                                                     Homo
                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                            anglogenesis-related
                                                                                                                                                                                                                                                                                                                                           22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                AAY53775 standard; Protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 347-348; 527pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to external signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-476052/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strabala TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity es 6; Conserv
                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 TGRIPP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TGRIPP 6
Tarli L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nieuwenhuizen
                                                      98US-0075338
99US-0300425
                                                                                                99WO-EP03210
Viti F,
                                                                                                                                                                                                                                blood vessel occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding a polypeptide involved in cell rating transgenic plants with modified responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                 marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          determining region (CDR) residues located at the periphery of the binding site. The improved antibody is used for rapid targeting markers of angiogenesis, for detecting diseases characterized by vascular proliferation, such as diabetic retinopathy, age related macular degeneration or tumours. The antibody localizes the respective tissue within 3 to 4 hours after injection. It is used in immunoscintigraphic detection of angiogenesis and for diagnosis and therapy of tumours and diseases characterized by vascular proliferation. The antibody can be conjugated to a molecule which induces blood coagulation and blood vessel occlusion. These conjugates are used in the preparation of injectable compositions for the treatment of angiogenesis-related pathologies, especially caused by or associated with ocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a modified human scFv antibody which has specific affinity for a characteristic epitope of the ED-B domain of fibronectin. The affinity of the antibody for this epitope was improved by introducing a number of mutations in the complementarity determining region (CDR) residues located at the periphery of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibronectin ED-B domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-039074/03
                                                                                                             21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amalgamation
              WPI;
                                                                                                                                                                                                                                                                           uveitis; endophthalmitis; bone; joint; central nervous system; Finflammatory lesion; acne vulgaris; enzyme linked immunosorbent dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU40893 standard; Protein;
                                                     Skeiky YAW,
                                                                                                                                                                  20-APR-2001;
                                                                                                                                                                                             01-NOV-2001
                                                                                                                                                                                                                        WO200181581-A2
                                                                                                                                                                                                                                                    Propionibacterium
                                                                                                                                                                                                                                                                                                                       SAPHO syndrome;
                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes immunogenic protein #1789
                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                       AAU40893;
                                          L'maisonneuve
N-PSDB; AAS59513.
                                                                                 (CORI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Page -;
              2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 6; Conser
                                                                                  CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGRIPP
                                                                                                           ; 2000US-199047P.
; 2000US-208841P.
; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                        Persing DH,
ve J, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                                                                                                                    2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227
                                                                                                                                                                                                                                                                                                                       synovitis; acne;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59pp;
                                                                                                                                                                                                                                                    acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       does not appear
sequences given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                     DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epitope specific antibodies and conjugate
                                          Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                        pustulosis; hypertosis; osteomyelitis;
joint; central nervous system; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the specification; it claim 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 238;
                                                           Bhatia
                                                           Α.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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Matches Query Match Best Local

Similarity 6; Conserv

100.0%; ilarity 100.0%; Conservative

0

Score 34; DB 22; Pred. No. 1.3e+02;

Length 307; Indels

0;

Gaps

0,

Sequence

AA;

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cc sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic cc polypeptides. The proteins and their associated DNA sequences are used in Cc the treatment, prevention and diagnosts of medical conditions caused by Cc P. acnes. The disorders include SAPHO syndrome (synovitis, acne, Cc pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. Cc P. acnes is also involved in infections of bone, joints and the central Cc presence or absence of P. acnes in a patient comprises contacting a Cc presence or absence of P. acnes in a patient comprises contacting a Cc sample with a binding agent that binds to the proteins of the invention Cc specific for P. acnes proteins. These antibodies can be used to compregulate expression and activity of P. acnes polypeptides and ctivity of P. acnes polypeptides and contactions. The antibodies can be used as therefore treat P. acnes infections. The antibodies may also be used as contaction agents for determining P. acnes presence, for example, by Cc enzyme linked immunosorbent assay (ELISA).

Cc Note: The sequence data for this patent did not form part of the printed contaction, but was obtained in electronic format directly from WIPO at form wino intrombynibitished pot sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                      ftp.wipo.int/pub/published_pct_sequences
         307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1069pp;
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RESULT 12
AAU14225
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                                                                                                                                                                                              Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antialtergic; dermatological; haemostatic; antialtergic; dermatological; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                                                                                                                                                                          AAU14225 standard;
                                                                                                                                                                                                                                                                          Human novel protein
                                                                                                                                                                                                                                                                                               24-OCT-2001
                                                                                                                     02-AUG-2001
                                                                                                                                            WO200155437-A2
                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                      tissue
                                                                                               25-JAN-2001; 2001WO-US02623
                                                    (HYSE-) HYSEQ
                                                                         25-JAN-2000; 2000US-0491404
                               YT,
                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                     1 TGRIPP 6
                                                                                                                                                                                      regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                 TGRIPP 89
                               Liu C,
                                                                                                                                                                                                                                                                                                (first
                                Drmanac
                                                                                                                                                                                                                                                                                                                                           Protein; 307
                                                                                                                                                                                                                                                                             #96.
                                                                                                                                                                                        immune disorder
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WPI; 2001-451939/48. N-PSDB; AAS22530.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides encoding novel human CC proteins or their active domains. The polypeptides, polynucleotides and cc antibodies raised against the polypeptides are used in a method of CC treatment of a mammal and prevention of disorders caused by the aberrant CC protein expression or activity. The polypeptides can be used as CC molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the CC polypeptides are used to identify compounds which bind to the CC production of recombinant proteins, and in generating anti-sense DNA or CC target drugs to a tumour, in assays to determine biological activity, to CC raise antibodies/elicit an immune response, to determine quantitative CC protein levels, as tissue markers, and to isolate receptors or ligands. CC plypeptides of the invention may also be useful in treating platelet CC disorders, stem cell disorders, regenerating bone, cartilage, tendon, the proliferation, differentiation and survival of stem cells, as a cc contraceptive, treating osteoporosis and osteoarthritis, anaemia, CC Alzheimer's, parkinson's and Huntington's diseases, amylotrophic lateral CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                             immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antialergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis
               (HYSE-) HYSEQ INC
                                               25-JAN-2000; 2000US-0491404
                                                                                      25-JAN-2001; 2001WO-US02623
                                                                                                                                                                WO200155437-A2
                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, alleray, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                         t188ue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU14227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU14227 standard; Protein; 312 AA
                                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                         Human novel protein #98.
                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                       regeneration;
                                                                                                                                                                                                                                                                                                                                                       novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGRIPP 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                        protein; Antianaemic; osteopathic; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 22; I
Pred. No. 1.3e+02;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                 asthma; osteoporosis;
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RESULT 14
AAU00443
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AC AAU0
DT 19-(
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KW Ma
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Best Local Similarity
""" 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides encoding novel human CC proteins or their active domains. The polypeptides, polynucleotides and cc antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as protein expression or activity. The polypeptides can be used as protein expression or activity. The polypeptides can be used as protein proteins, and in antibody production. The polypeptides are used to identify compounds which bind to the prolypeptides. Polynucleotides of the invention are used as probes and production of recombinant proteins, and in generating anti-sense DNA or the production of recombinant proteins, and in generating anti-sense DNA or the transport of the invention can be used to car at the discrete transport of the invention are creeptors or ligands are antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. CC protein levels, as tissue markers, and to isolate receptors or ligands. CC protein levels, as tissue markers, and to isolate receptors or ligands. CC protein levels, as tissue markers, and to isolate receptors or ligands. CC protein levels, as tissue markers, and to isolate receptors or ligands. CC disorders, retem cell disorders, regenerating bone, cartilage, tendon, cc ligament and/or nerve tissue, wound healing, treating burns, promoting cc the proliferation, differentiation and survival of stem cells, as a cc ligament and/or nerve tissue, wound healing, treating burns, promoting cc contraceptive, treating osteoporosis and survival of stem cells, as a clerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, cc anti-inflammatory disease, eczema, haemophilia, thrombosis, and infection.

The present sequence represents a protein of the invention.
                                                          09-SEP-1999;
                                                                                                  06-SEP-2000;
                                                                                                                                                                                                                                                      Malze; plant disease resistance; crop; soybean; sunflower; sorghum; canola; wheat; alfalfa; cotton; rice; barley; millet; plant cell death; herbicide resistance; ZmLRR1-1; Cf-2; Cf-9.
                                                                                                                                                                                                                                                                                                                                         Maize disease resistance enhancing protein ZmLRR1-1.
                                                                                                                                           15-MAR-2001
                                                                                                                                                                                    WO200118061-A2.
                                                                                                                                                                                                                            Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU00443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU00443 standard; Protein; 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 576-577; 894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptides useful nervous system disorders, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-451939/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGRIPP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 AA;
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                                                                                               2000WO-US24403
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                             99US-0152988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating anti-inflammatory diseases, for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 312;
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(PION-) PIONEER HI-BRED INT INC

N-PSDB;

2001-226742/23.

AAS01013.

Simmons CR

N-PSDB; ABL09845

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cc a Zea mays gene homologue for a leucine-rich repeat (LLR) containing CC disease resistance gene of the Cf-2 or Cf-9 type. These novel maize CC enhancing disease resistance in crops and transgenic plants including CC enhancing disease resistance in crops and transgenic plants including CC maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley or millet. The level of disease resistance protein is increased CC by transforming a plant cell with a recombinant expression cassette CC which comprises the disease resistance polynucleotide operably linked to a promoter, or by culturing the plant cell under plant growing conditions CC to produce a regenerated plant, or by inducing expression of the CC polynucleotide to modulate the disease resistance protein in a plant. CC for increasing resistance in a plant to disease, controlling cell death, CC and conferring resistance to herbicides. They are useful as probes or confident transcripts. They can be used for recombinant expression of the conference of antibodies, and in sense or antisense suppression of the polynucleotide in a host cell, tissue or plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated maize disease resistance polynucleotide useful for increasing resistance in a plant to disease, controlling cell death, and conferring resistance to herbicides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence representing maize ZmLRR1-1 protein is 1 of 7 novel disease resistance proteins (AAU00443-AAU00449). The ZmLRR1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 24018
                                                                                            23-MAR-2000;
11-JUL-2000;
                                                                                                                                       23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                     27-SEP-2001
                                                                                                                                                                                                   WO200171042-A2
                                                                                                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                            pharmaceutical.
                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                   ABB65742;
                                                                                                                                                                                                                                                                                                                                                                                                ABB65742 standard; Protein;
                                  Venter JC, Adams M,
                                                             (PEKE ) PE CORP NY
   2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 TGRIPP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative 0;
                                                                                          2000US-191637P.
2000US-0614150.
                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                    Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                   334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB
Pred. No. 1.4
); Mismatches
                                  Myers
                                      E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 1.4e+02; ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 330;
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Search completed: August 20, 2003, 12:33:49
Job time : 14.1928 secs

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                                                Query Match
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Thes 6; Conserve
                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions - \,
                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 24018; 21pp + Sequence Listing; English
                                                                                                                                 Sequence
 231 TGRIPP 236
                              1 TGRIPP 6
                                                                                                                                   334 AA;
                                                                Conservative
                                                                                100.0%;
                                                                     0;
                                                                 Score 34; DE
Pred. No. 1.4
D; Mismatches
                                                                                   1.4e+02;
                                                                                                     DB
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                                                                                                     Length 334;
                                                                        Indels
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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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    protein search, using sw model

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1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

3: /cgn2_6/ptodata/1.

4: /cgn2_6/ptodata/1.

5: /cgn2_6/ptodata/1.

5: /cgn2_6/ptodata/1.
                                                                                                                                                                                                                                                                                                          Query
Match
     328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-512-082-34
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                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
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     196
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 US-08-605-150A-6
US-08-605-150A-6
US-08-244-646-17
US-08-244-646-17
US-08-244-646-17
US-08-244-646-17
US-08-244-646-17
US-08-248-646-12
US-08-881-706-2
US-09-881-706-2
US-09-397-238A-12
US-09-397-238A-12
US-09-252-991A-20481
US-09-252-991A-24538
US-09-252-991A-24538
US-09-252-991A-217863
US-09-252-991A-18178
US-09-252-991A-18178
US-09-252-991A-23172
US-09-252-991A-18172
US-09-252-991A-18172
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Sequence
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Sequence
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Sequence
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Sequence
Sequence
Sequence
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32, Appl
21784, A
27863, A
12988, A
23179, A
23122, A
25576, A
18172, A
19978, A
                                                                                            92, Appl
29189, A
24538, A
                                                                                                                            12, App1
20481, A
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2, Appli
12, Appl
12, Appl
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2, Appli
17, Appl
15, Appl
21, Appl
                                                                                                                                                                                                                                                83, Appl
24232, A
26457, A
31991, A
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US-09-228-986-83
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	888888888888888888888888 5555555555555
	287 390 396 410 410 421 421 421 523 523 523 528 918 985
	444411000444004
ALIGNMENTS	US-09-252-991A-24517 US-09-252-991A-24697 US-09-252-991A-18709 US-08-123-343A-7 US-09-431-573-4 US-09-431-573-5 US-09-431-573-5 US-09-252-991A-25017 US-09-252-991A-25018 US-08-473-553A-8 US-09-252-991A-25851 US-09-252-991A-25854 US-09-252-991A-28544 US-09-252-991A-28549 US-08-473-553A-2
	Sequence 21133, A Sequence 24517, A Sequence 24697, A Sequence 18709, A Sequence 5, Appli Sequence 7, Appli Sequence 5, Appli Sequence 30742, A Sequence 30742, A Sequence 3101B, A Sequence 3101B, A Sequence 25851, A Sequence 25851, A Sequence 25851, A Sequence 25851, A Sequence 27, Appli

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Sequence 83, Application US/09228986

Patent No. 6359198

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: And Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 83
LENGTH: 153
TYPE: PRT
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-24232
; Sequence 24232, Application US/09252991A
; Patent No. 6551795
US-09-252-991A-24232
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                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
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                        APPLICANT: MAIC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AEBUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196,136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR TILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24232

LENGTH: 457

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 TGRIPP 131
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Pred. No.
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PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26457

LENGTH: 10
                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31991
LENGTH: 308
TYPE: PRT
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US-09-252-991A-26457
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/74,788 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                              Local Similarity hes 5; Conserv
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5. 6551795
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5; Conserv
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83.3%;
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Pred. No.
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Pred. No. 52;
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Pred. No.
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                                                                                    DB
81;
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US-08-605-150A-6
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                                                                                                                                                                                                    Sequence 2, Application US/08605150A Patent No. 6103520
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 367 amino acid
                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                         APPLICANT: Topfer, Reinha
APPLICANT: Hausmann, Ludg
APPLICANT: Schell, Jozef
TITLE OF INVENTION: GLYCE
TITLE OF INVENTION:
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APPLICANT: Schell, Jozef
APPLICANT: Schell, JOZEF
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APPLICATION NUMBER: PCT\EP94\02936
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4329827.3
FILING DATE: 03-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-854-5502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Klein & Szekeres
                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Irvine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 01-MAI
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nes 5; Conserv
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                                           STREET:
COUNTRY:
               STATE:
                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                     347 TGRLPP 352
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amino acid
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                              Irvine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4199 Campus Drive, Suite 700
             CA
                                             4199 Campus Drive, Suite 700
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                                                                                                                                                                         Topfer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                   94.1%;
                                                                                                                           GLYCEROL-3-PHOSPHATE DEHYDROGENASE
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFOR APPLICANT:
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,646
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
000915
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: PCT\EP94\02936
FILLING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                         STREET: 5370 M
CITY: Boulder
STATE: CO
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ent No.
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ATTORNEY/AGENT INFORMATION:
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                                                         FILING DATE: 06-JUN-1994
                                                                                                                                                                                  COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Szekeres, Gabor L.
REGISTRATION NUMBER: 28,675
REFERENCE/DOCKET NUMBER: 54
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CLASSIFICATION:
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                                                                                                                                                                                                                                      E: Sally A. Sullivan
5370 Manhattan Circle Suite 201
                                                                                                                                                                                                                                                                                                                                  Bergmann,
                                                                                                                                                                                                                                                                                                                                                  Darvill, Alan
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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06-DEC-1991
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                                                                                                                                                                                                                                                                                          Endopolygalacturonase Inhibitor
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RESULT 8
US-08-244-646-15
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                                                                                                                                                APPLICATION NUMBER: IT RM 91A 000915
FILING DATE: 06-DEC-1991
PRIOR PAPELICATION DATA:
                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                            NAME: Sullivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                              FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleotide Sequences Coding An TITLE OF INVENTION: Endopolygalacturonase Inhibitor NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 80303
                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/244,646 FILING DATE: 06-JUN-1994 CLASSIFICATION: 435
              TELEPHONE:
                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sullivan, Sally A. REGISTRATION NUMBER: 32,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: WO F
FILING DATE: 04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Sally A. Sullivan
5370 Manhattan Circle Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                     S
(303)499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bergmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De Lorenzo, Giulia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salvi, Giovanni
Albersheim, Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Darvill, Alan
                (303)499-8080
                                                                                                                     UMBER: WO PCT/IT/00158
04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Felice
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INFORMATION FOR SEQ ID NO:

15:

SEQUENCE CHARACTERISTICS:

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; MOLECULE TYPE: protein US-08-244-646-15
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US-08-592-936B-21
                                            RESULT 10
US-09-111-573-21
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               Patent No.
                            Sequence 21,
                                                                                                                                                                  Matches
                                                                                                                                                                                              Query Match
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APPLICANT: Kellogg, CAPPLICANT: Bestwick,
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (650) 324-09 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,936B FILING DATE: 29-JAN-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 4257-0012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bestwick, Richard K.
TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR
TITLE OF INVENTION: REGULATED EXPRESSION OF TRANSGENES IN PLANTS
                                                                                                                                                                                                                                                                                 MOLECULE TYPE: PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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mes 5; Conserv
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                                                                                                       216 TGKIPP 221
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                                                                                                                                                                                                                                                                                                                               amino acid
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                             Application US/09111573
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350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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83.3%;
                                                                                                                                                                                91.2%;
83.3%;
                                                                                                                                                                                                                                        predicted amino acid of SEQ ID NO:20
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Pred. No. 1.4e+02;
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GENERAL INFORMATION:
APPLICANT: Chong, Joane
APPLICANT: L1, Jianming
ITTLE OF INVENTION: Receptor Kinase BIN1
FILE REFERENCE: 07251/022001
CURRENT APPLICATION NUMBER: US/08/881,706
CURRENT FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-09-111-573-21
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Best Local Similarity
Watches 5; Conservi
                                               ; TYPE: PRT; ORGANISM: Arabidopsis sp. US-08-881-706-2
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Patent No. 6245969
Query Match
Best Local Similarity
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APPLICATION NUMBER: US/08/592

APPLICATION NUMBER: US/08/592

FILING DATE: 29-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: EVANS, SUSAN T.

REGISTRATION NUMBER: 38,443

REFERENCE/DOCKET NUMBER: 4257

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650).324-0880

TELEPHONE: (650).324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 324-090 INFORMATION FOR SEQ ID NO:
                                                                                                  LENGTH: 1196
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
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LENGTH: 342 amino acid
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
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                                                                                                                                                                                                                                                                                                                                                                                                      216 TGKIPP 221
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Bestwick, Richar
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91.2%;
83.3%;
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Pred. No. 1.4e+02;
Score 31; DB 3; Pred. No. 4.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid coding sequence NO:20
                Length 1196;
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                                                                                                                                              Sequence 12, Application US/09188469 Patent No. 5989825 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO:
                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,569A FILING DATE: 10.0CT-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: NO. 58829260an, Kevin E REGISTRATION NUMBER: 35,303 REFERENCE/DOCKET NUMBER: 93,509-F
                                                    TITLE OF INVENTION: Excitato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                                         JUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Excitato
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                       171 TGKVPP 176
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                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                  564 amino acids
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                                                               /EKAVAnaugh, Michael P
//ENTION: Excitatory Amino Acid Transporter Genes
                                                                                                  Arriza, Jeffrey L
Ellasof, Scott
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                Amara, Susan G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kavanaugh,
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Arriza, Jeffrey L
Eliasof, Scott
                                                                                                                                                                                                                                                                                                                                                                                                        linear
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       McDonnell Boehnen Hulbert & Berghoff
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                          ADDRESS
                                                                                                                                                                                                                                                                                                                            88.2%;
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Pred. No.
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US-09-188-469-12
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09397238A Patent No. 6284505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08
FILING DATE: 10-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: No. 599825nan, Ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US/08/948,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Til
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
       APPLICATION NUMBER: US/09/397,238A
FILING DATE: 16-Sep-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6284505nan, Kevin E
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Amara, Susan G
Arriza, Jeffrey L
Ellasof, Scott
                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Excitatory
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 TGKVPP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: protein
                                                                                                                                                                                                 ZIP: 60606
                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                   ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 South Wacker Drive
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                                                                                                                                                                                                                                                          300 South
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66.7%;
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                                                                                                                                                                                                                                                                                                                   and Uses
                                                                                                                                                                                                                                                                                                                                               Michael P
NUMBER: 93,509-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kevin E
                                                                                                                                                                                                                                                        Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93,509-F
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Pred. No.
                                                                                                                                                                                                                                                                                                                            Amino Acid Transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5e+02;
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RESULT 15
US-09-252-991A-20481
; Sequence 20481, Application US/09252991A
; Patent No. 6551795
; Patent TON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-397-238A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
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                                                                                                                                                                                                                                        ; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (388)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-20481
                                                                                                                   Ş
Search completed: August 20, 2003, 12:44:23 Job time : 4.15663 secs
                                                                                 밁
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20481
LENGTH: 582
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
FRAVURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 88.2%;
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                           Query Match 88.2%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 TGKVPP 176
                                                                                 94 TGRFPP 99
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                                                                                                                         1 TGRIPP 6
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Pred. No. 3.5e+02;
2; Mismatches 0; Indels
                                                                                                                                                               Score 30; DB 4; Length 582;
Pred. No. 3.6e+02;
0; Mismatches 1; Indels
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 2000000000
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Match
      August 20, 2003, 12:40:51; Search time 6.50602 Seconds (without alignments) 121.698 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003
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119
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1 US-09-300-425B-34
1 US-09-300-425B-21
5 US-10-101-464A-83
5 US-10-101-464A-83
5 US-10-101-464A-766
5 US-10-101-464A-751
5 US-10-101-464A-894
5 US-10-101-464A-894
5 US-10-101-464A-891
5 US-10-101-464A-891
6 US-10-101-464A-891
1 US-09-823-394-2
1 US-09-864-73-394-2
1 US-09-864-73-394-2
1 US-09-864-758-269-14
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Compugen Ltd
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   Sequence 344, App Sequence 944, App Sequence 944, App
                                                                                                                                                                                                                                             Description
                                                                         Sequence
Sequence
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Sequence 2, A
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                                                      e 34, Appl
e 21, Appl
e 65, App
e 83, Appl
e 645, App
e 645, App
e 766, App
e 776, App
e 771, App
e 8911, App
e 8911, App
e 701, App
e 701, App
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0-219-479-	S-10-219-46	0-219-464-	-10-219-075-	-10-219-003-	-10-230-434-	19-076-	-10-227-883-	-10-227-873-	-10-218-849-6	-10-216-159A	-10-230-414-	-10-218-631-	-10-230-338-	0-230-163-	227-884-	-10-216-163-6	8-626-	16-664-2	8-605-	-09-764-891-4	-464A-	-10-101-464A-631	0-156-761-	-10-156-761-1423	-10-080-170-290	-10-101-464A-57	-10-101-464A-5	-10-101-464A-92	US-10-101-464A-896
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## ALIGNMENTS

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Publication NU.

GENERAL INFORMATION:

APPLICANT: NERI, Dario

APPLICANT: TARLI, Lorenzo

APPLICANT: TARLI, Lorenzo

APPLICANT: VITI, Francesca

APPLICANT: VITI, Francesca

APPLICANT: BIRCHLER, Manifred

TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES

TITLE OF INVENTION: ANGIOGENESIS

FILE REFERENCE: SCH-1739P1

CURRENT APPLICATION NUMBER: US/09/300,425B

PRIOR APPLICATION NUMBER: 09/075,338

PRIOR PEPLICATION NUMBER: 09/075,338

PRIOR FILING DATE: 1998-05-11

NUMBER: 09 SEQ ID NOS: 34
В
                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 34

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B

OTHER INFORMATION: antibody clone
US-09-300-425B-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-09-300-425B-34
                                                                                              Query Match
Best Local :
                                                                               Matches
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1 TGRIPP 6
                                     1 TGRIPP 6
                                                                         6; Conserv
                                                                   100.0%; Score 34; DB 11; llarity 100.0%; Pred. No. 4.4e+05; Conservative 0; Mismatches 0;
                                                                                                         Length 6;
                                                                     Indels
                                                                   0;
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RESULT 2

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US-09-300-425B-21; Sequence 21, Application US/09300425B; Publication No. US20030045681A1
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US-10-101-464A-685
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                                 Qy
                                                                                                                                              ; ORGANISM: Pinus radiata US-10-101-464A-685
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SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 685, Application US/10101464A Publication No. US20030046728A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF INVENTION: ANGIGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 11000.1020c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: VL antibody OTHER INFORMATION: specific for ED-B domain of fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                     LENGTH: 10
TYPE: PRT
                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-01-11
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                                                                                                                                                                                                                          ID NO 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                           Local
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                                       1 TGRIPP 6
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                                                                        Similarity 6; Conserv
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 TGRIPP 26
                                                                        100.0%; ilarity 100.0%; Conservative 0
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                                                                                             Score 34; DB Pred. No. 29;
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                                                                                                                 DB 15;
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                                                                            ; ORGANISM: Eucalyptus grandis US-10-101-464A-645
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Best Local :
                                                                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 645
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APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
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PRIOR PELICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR EPLICATION NUMBER: PCT/US00/00724
PRIOR EPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
Matches
                 Query Match
Best Local
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/162,866 PRIOR FILING DATE: 1999-11-01
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
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PRIOR FILING DATE: 2000-11-01
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                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US00/00724
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                                                                                                                                          LENGTH:
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                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nieuwenhuizen, Nicolaas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Timothy
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                       100.0%;
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Pred. No. 40;
                       Score 34;
Pred. No.
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      mismatches
                                              DB 15; Length 155;
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        Indels
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1 TGRIPP 6

|||||| TGRIPP 121

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; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-751
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CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR PPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-00-11
PRIOR FILING DATE: 2000-00-11
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; Sequence 766, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
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  Query Match
Best Local Similarity
                                                                                                                                        NUMBER OF SEQ ID NOS: 989
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 751
LENGTH: 224
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APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, N APPLICANT: Higgins, Colleen
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TYPE: PRT
ORGANISM: Pinus radiata
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SOFTWARE: FastSEQ for Windows Version 4.0
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  100.0%;
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Score 34;
Pred. No.
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Pred. No. 42;
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DB 15;
58;
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                   Length 224;
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                               ; ORGANISM: Streptomyces avermitilis US-10-156-761-8911
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US-10-101-464A-894
; Sequence 894, Application US/10101464A
; Sequence 894, US20030046728A1
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CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 09/162,866
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
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                                                                         NUMBER OF SEQ ID NOS:
SEQ ID NO 8911
LENGTH: 598
TYPE: PRT
Query Match
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 894
LENGTH: 705
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Best Local
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, N
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TYPE: PRT
ORGANISM: Pinus radiata
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HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                    SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
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Pred. No. 1
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1.7e+02;
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94.18;

Score 32;

DB

15;

Length 598

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US-10-101-464A-701
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US-10-101-464A-898
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cell Signaling
TITLE OF INVENTION: And Their, Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION. And Their, Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION.
THE OF THE OBJECT ON ORDER: US/10/101,464A
CURRENT PILING DATE: 2002-03-18
PRIOR APPLICATION UNMBER: 09/704,302
PRIOR APPLICATION UNMBER: 09/228,986
PRIOR APPLICATION UNMBER: 60/162,866
PRIOR FILING DATE: 1999-01-01
PRIOR APPLICATION UNMBER: PCT/US00/00724
PRIOR APPLICATION UNMBER: PCT/US00/00724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 898, Application US/10101464A
Publication No. US20030046728A1
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APPLICANT: Higgins, Colleen M.
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                                                                   SEQ ID NO 898
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
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SOFTWARE: FastSEQ for
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                                                                                  NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                             PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
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ORGANISM: Pinus radiata
                          TYPE: PRT
                                          ENGTH: 383
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nes 5; Conservative
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83.3%;
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l; Mismatches
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Pred. No.
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thes 0;
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1.4e+02;
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US-10-101-464A-898
          PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33825, Application US/09864761 Patent No. US20020048763A1
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Best Local
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PRIOR FILING DATE: 1997-06-24
NUMBER OF SEC. TO
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APPLICANT: Salk Institute for Biological Studies
TITLE OF INVENTION: RECEPTOR KINASE, BIN 1
FILE REFERENCE: SALKINS.012CP1
CURRENT APPLICATION NUMBER: US/09/823,394
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-864-761-33825
                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-55-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
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                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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TYPE: PRT
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Chen, Wensheng
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2001-01-30
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83.3%;
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Pred. No. 3.5e+02;
1; Mismatches 0
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Pred. No.
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CURRENT APPLICATION NUMBER: US/10/101,464A CURRENT FILING DATE: 2002-03-18 PRIOR APPLICATION NUMBER: 09/704,302 PRIOR FILING DATE: 2000-11-01 PRIOR APPLICATION NUMBER: 09/228,986 PRIOR FILING DATE: 1999-01-12 PRIOR APPLICATION NUMBER: 60/162,866 PRIOR FILING DATE: 1999-11-01 PRIOR APPLICATION NUMBER: 60/162,866 PRIOR FILING DATE: 1999-11-01 PRIOR APPLICATION NUMBER: PCT/US00/00724 PRIOR FILING DATE: 2000-01-11
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33825
LENGTH: 63
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Best Local
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                        APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
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OTHER INFORMATION: E
OTHER INFORMATION: E
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OTHER INFORMATION: E
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PRIOR FILING DATE: 2001-01-29
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FastSEQ for Windows Version 4.0
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| SGRIPP 35
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5; Conserv
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EST_HUMAN
SWISSPROT
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EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
EXPRESSED IN HELA, SIGNAL = 2.1
EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXPRESSED IN LUNG, SIGNAL = 1.1
EXPRESSED IN PLACENTA, SIGNAL = 1.1
EXPRESSED IN BT474, SIGNAL = 8.4
EXPRESSED IN BT474, SIGNAL = 8.4
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83.3%;
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HEART, SIGNAL = 1.3
T: A1243801.1, EVALUE 8.60e+00
T: Q13085, EVALUE 1.00e-30
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Search completed: August 20, 2003, 13:16:48 Job time: 7.50602 secs

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US-09-758-269-14
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US-09-758-269-14
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                                                          Matches
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Best Local Similarity bs...
Thes 5; Conservative
                                                                     Query Match
Best Local
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SEQ ID NO 14
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LENGTH: 370
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09758269 Patent No. US20020104120A1
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/758,269
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: JP 2001-003476
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: JP 2000-010056
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEO ID NOS: 33
                                                                                                                                                                                                                                                                                                  APPLICANT: KOBAYASHI, MASATOMO
APPLICANT: SHINOZAKI, KAZUO
TITLE OF INVENTION: TRANSGENIC PLANTS CARRYING NEOXANTHIN
TITLE OF INVENTION: CLEAVAGE ENZYME GENE
FILE REFERENCE: 3914-3
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: IUCHI, APPLICANT: KOBAY
                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
142 SGRIPP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 TGQIPP 359
                            1 TGRIPP 6
                                                                                                                                                       604
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                                                       Similarity 5; Conserv
                                                                                                                                                                                    PatentIn Ver. 2.1
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                       SATOSHI
                                                                   88.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.2%;
83.3%;
                                                    Score 30; DB 10;
Pred. No. 8.4e+02;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2e+02;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence:
                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                          Score
        100.0
                                                                                     Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                    Query
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/cgn2_6/ptodata/1/paa/US091_COMB.pep:*
/cgn2_6/ptodata/1/paa/US092_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US095_COMB.pep:*
/cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
/cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
/cgn2_6/ptodata/1/paa/US097B_COMB.pep:*
/cgn2_6/ptodata/1/paa/US098_COMB.pep:*
/cgn2_6/ptodata/1/paa/US098_COMB.pep:*
/cgn2_6/ptodata/1/paa/US098_COMB.pep:*
/cgn2_6/ptodata/1/paa/US098_COMB.pep:*
/cgn2_6/ptodata/1/paa/US101_COMB.pep:*
/cgn2_6/ptodata/1/paa/US101_COMB.pep:*
/cgn2_6/ptodata/1/paa/US101_COMB.pep:*
/cgn2_6/ptodata/1/paa/US104_COMB.pep:*
/cgn2_6/ptodata/1/paa/US104_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US083_COMB.pep:*
/cgn2_6/ptodata/1/paa/US084_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US087_COMB.pep:*
/cgn2_6/ptodata/1/paa/US088_COMB.pep:*
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     US-09-075-338C-34
US-09-300-425B-34
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                                                                         Description
Sequence 34,
Sequence 34,
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## ALIGNMENTS

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RESULT 1
US-09-075-338C-34

(Sequence 34, Application US/09075338C
Sequence 34, Application US/09075338C

(SEMERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
COMPLICANT: NERI, Dario
APPLICANT: NERI, Lorenzo
APPLICANT: VITI, Francesca
APPLICANT: HIRCHLER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
FILE REFERENCE: SCH-1733
CURRENT PAPLICATION NUMBER: US/09/075,338C
CURRENT FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
CURRENT FILING DATE: 1998-05-11
SEQ ID NO 34
CHERCIPH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: anti-ED-B
OTHER INFORMATION: antibody clone
US-09-075-338C-34

Query Match
Best Local Similarity 100.0%; Pred. No. 5.2e+06;
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                                   ; FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B; OTHER INFORMATION: antibody clone
US-09-512-082-34
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SEQ ID NO 34
LENGTH: 6
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Best Local :
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Query Match
                                                                                                                                                               SEQ ID NO 34
                                                                                                                                                                                                                                                                                APPLICANT: TARLÍ, LOTENZO
APPLICANT: VITI, FRANCESCA
APPLICANT: BIRCHLER, MANÍTED
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: SCH-1733P2
CURRENT APPLICATION NUMBER: US/09/512,082
CURRENT FILING DATE: 2000-02-24
CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGIGENESIS
                                                                                                                                                                                           PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-(
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-
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                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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les 6; Conserv
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VITI, Francesca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NERI, Dario
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Pred. No.
   Score 34;
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; OTHER INFORMATION: Description of Artificial Sequence: VL antibody ; OTHER INFORMATION: specific for ED-B domain of fibronectin US-09-075-338C-21
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; GENERAL INFORMATION:
; APPLICANT: NERI, Da
; APPLICANT: TARLI, L
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δõ
                                                                                                     US-09-300-425B-21
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SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 21
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VITI, Francher, APPLICANT: BIRCHLER, TITLE OF INVENTION: OF INVENTION: OF INVENTION: OF INVENTION: OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/09300425B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MARLI, Lorenzu APPLICANT: VIII, Francesca APPLICANT: BIRCHLER, Manfred TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY SPERRENCE: SCH-1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100. Matches 6; Conservative
                                                                                                                                                                                                                    SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local (
                                 Matches
                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                  ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: VL antibody OTHER INFORMATION: Specific for ED-B domain of fibronectin
                                                                                                                                                                                   LENGTH: 108
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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1 TGRIPP 6
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VITI, Francesca
BIRCHLER, Manfred
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                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                 100.0%; Score 34; DB 17; 100.0%; Pred. No. 4.8e+02;
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Pred. No. 4.8
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                                                                                                                                                            ; ORGANISM: Pinus radiata
PCT-US00-00724-685
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                                                                                                                                                                                                  SEQ ID NO 685
LENGTH: 109
TYPE: PRT
                                                                                            Query Match
Best Local
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LENGTH: 108
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: PCT/US00/00724
CURRENT FILING DATE: 2000-01-11
EARLIER APPLICATION NUMBER: 09/228,986
EARLIER FILING DATE: 1999-01-12
EARLIER APPLICATION NUMBER: US 60/162,866
EARLIER FILING DATE: 1999-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020C1PCT
                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1322
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, Nicolaas
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PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGIOGENESIS FILE REFERENCE: SCH-1733P2 CURRENT APPLICATION NUMBER: US/09/512,082 CURRENT FILING DATE: 2000-02-24 DBTOB ADDITOR TO NUMBER: 0000-02-24
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21 TGRIPP 26
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                                   1 TGRIPP 6
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UTTI, Francesca
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                                                                           Conservative
                                                                                            100.0%;
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Pred. No.
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RESULT 10
US-60-162-866-685
; Sequence 685, Application US/60162866
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
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Best Local Similarity
"atches 6; Conserve
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GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c1U
CURRENT APPLICATION NUMBER: US/09/704,302A
CURRENT FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 1402
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 685
LENGTH: 109
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LENGTH: 109
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Best Local :
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APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/218,986
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 09/162,866
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 050/162,866
PRIOR FILING DATE: 1999-11-01
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SOFTWARE: FastSEQ for
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                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pinus
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Pred. No. 4.8e+02;
Pred. No. 4.8e+02;
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Pred. No.
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; ORGANISM: Pinus radiata
US-60-162-866-685
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US-09-513-999C-4223
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SEQ ID NO 685
LENGTH: 109
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APPLICANT: Dumas Milne Edwards, J.B.
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SEQ ID NO 167644
LENGTH: 114
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Best Local Similarity
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                                SOFTWARE: Patent.pm
SEQ ID NO 4223
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                                                                 CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681
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CURRENT APPLICATION NUMBER: US/60/162,866
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 1275
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CURRENT FILING DATE: 2003-04-28
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TITLE OF INVENTION: Soy uncleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                 APPLICANT: Duclert, A.
APPLICANT: Giordano, Jry.
TITLE OF INVENTION: Expressed Sequence Tags and
FILE REFERENCE: 59.US2.REG
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LOCATION: (1)..(114)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
PAT MRT3847 12239
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TYPE: PRT
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                 LENGTH: 144
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Pred. No.
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Pred. No. 4.8e+02;
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US-09-704-302A-83
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PCT-US00-00724-83
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                                  US-09-704-302A-83
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 83
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GENERAL INFORMATION:
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                                                                                                   SEQ ID NO 83
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                                                                                                                                                                                     TITLE OF INVENTION: Compositions Isolated from Plant Cells TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling FILE REFERENCE: 11000.1020clU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: PCT/US00/00724 CURRENT FILING DATE: 2000-01-11 EARLIER APPLICATION NUMBER: US 09/228,986 EARLIER FILING DATE: 1999-01-12 EARLIER APPLICATION NUMBER: US 60/162,866 EARLIER FILING DATE: 1999-11-01
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                                                                                                                  NUMBER OF SEQ ID NOS: 1402
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                         APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, Ni
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/704,302A CURRENT FILING DATE: 2002-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: -27..-1
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 153
TYPE: PRT
ORGANISM: Pinus radiata
                                               ORGANISM: Pinus
                                                                   TYPE: PRT
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                                                                                 LENGTH: 153
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Local Similarity 100.0%;
nes 6; Conservative 0
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                                                radiata
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Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1;
Pred. No. 6.7e+02;
Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
34;
DB
21;
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Length 153;
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GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.

ITILE OF INVENTION: and Their Use in the Modification of Plant Cells
ITILE OF INVENTION: compositions Isolated from plant Cells
ITILE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT APPLICATION NUMBER: US/704,302
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63
LENGTH: 153
TYPE: PRT
ORGANISM: Pinus radiata
US-10-101-464A-83
Search completed: August 20, 2003, 13:13:46 Job time: 62.4096 secs
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US-10-101-464A-83
I Sequence 83, Application US/10101464A
GENERAL INFORMATION:
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                                                                                                                                                                                     Query Match 100.0%; Score 34; DB 27; Length 153; Best Local Similarity 100.0%; Pred. No. 6.7e+02; Matches 6; Conservative 0; Mismatches 0; Indels
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                                                                                                1 TGRIPP 6
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126 TGRIPP 131
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126 TGRIPP 131
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Minimum DB :
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Perfect score:
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length: 2000000000
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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Maximum Match 100%
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   US-10-612-783-4490
US-10-408-765A-2802
US-10-266-897-3022
US-10-258-998A-5022
US-10-258-998A-6594
US-10-613-520-1396
US-10-613-520-1396
US-10-613-520-1397
US-09-674-546A-1527
US-09-674-546A-1529
US-10-603-108-3445
PCT-US03-20480-18
PCT-US03-20480-15
US-10-293-244-3884
US-10-293-244-3884
US-10-293-898A-6954
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US-10-336-041A-12

US-10-336-041A-12

US-10-336-041A-13

US-10-336-041A-13

US-10-336-041A-2
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US-10-408-765A-1931
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11, Appl
13, Appl
9, Appl
132, App
1331, App
1331, App
134, App
24490, Ap
24490, Ap
2594, Ap
6594, Ap
1196, Ap

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10, Appl
12, Appl
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US-10-273-573-6504	PCT-US03-23932-5	PCT-US03-23932-4	PCT-US03-23932-3	PCT-US03-23932-2	PCT-US03-23932-1	US-10-293-244-3552	US-10-273-573-5774	US-10-601-837-73	US-10-273-573-10255	US-10-408-765A-1449	US-10-293-244-1775	US-10-603-114-6114	US-10-293-244-3743	US-10-293-244-1916	US-10-258-898A-3366	US-10-286-897-3366	US-10-603-108-3272	PCT-US03-20480-16
650	<u>ن</u>	Sequence 4, Appli	Sequence 3, Appli	N	Sequence 1, Appli	Sequence 3552, Ap	Sequence 5774, Ap		10255,	Sequence 1449, Ap	1775,	6114,	Sequence 3743, Ap		Sequence 3366, Ap	Sequence 3366, Ap	72	Sequence 16, Appl

## ALIGNMENTS

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Sequence 1, Application US/10336041A
GENERAL INFORMATION:
APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis and
FILE REFERENCE: 27041-WOAS
CURRENT APPLICATION NUMBER: US/10/336,041A
CURRENT APPLICATION NUMBER: EP02 000 315.8
PRIOR APPLICATION NUMBER: EP02 000 315.8
PRIOR FILING DATE: 2002-01-03
PRIOR FILING DATE: 2002-00-03
PRIOR FILING DATE: 2002-02-25
NUMBER OF SEQ ID NOS: 13
SECTION NO.
RESULT 2
US-10-336-041A-10
; Sequence 10, Application US/10336041A
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: recombinant; OTHER INFORMATION: antibody fragment US-10-336-041A-1
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US-10-336-041A-1
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LENGTH: 238
TYPE: PRT
                                                                                                                                                                                        Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE LOCATION: (131)..(238) OTHER INFORMATION: VL
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE
LOCATION: (117)..(130)
OTHER INFORMATION: Linker
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SITE LOCATION: (1)..(116) OTHER INFORMATION: VH
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222 TGRIPP 227
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GENERAL INFORMATION:
APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis
FILE REFERENCE: 27041P_WOAS
                                                                                                                                      Sequence 11, Application US/10336041A GENERAL INFORMATION:
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SEQ ID NO 12
LENGTH: 240
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SEQ ID NO 10
LENGTH: 240
TYPE: PRT
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Best Local :
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Best Local :
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APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis and treatment of tumours
FILE REFERENCE: 27041p. WOAS
CURRENT APPLICATION NUMBER: US/10/336,041A
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: EPO2 000 315.8
PRIOR FILING DATE: 2002-01-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/336,041A CURRENT FILING DATE: 2003-01-03 PRIOR APPLICATION NUMBER: EP02 000 315.8 PRIOR ETILING DATE: 2002-01-03 PRIOR APPLICATION NUMBER: US60/358702 PRIOR APPLICATION NUMBER: US60/358702 PRIOR ETLING DATE: 2002-02-25
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CURRENT APPLICATION NUMBER: US/10/336,041A
CURRENT FILING DATE: 2003-01-03
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TITLE OF INVENTION: New methods for diagnosis
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220 TGRIPP 225
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Best Local Similarity
Watches 6; Conserve
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NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 11
LENGTH: 241
                                                                                                                                                                                                                                    Sequence 9, Application US/10336041A GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 247
                                                                      CURRENT APPLICATION NUMBER: US/10/336,041A CURRENT FILING DATE: 2003-01-03 PRIOR APPLICATION NUMBER: EP02 000 315.8 PRIOR FILING DATE: 2002-01-03 PRIOR APPLICATION NUMBER: US60/358702 PRIOR EILING DATE: 2002-02-25
                                                                                                                                                                                   APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis
FILE REFERENCE: 27041P_WOAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis and treatment of tumours
FILE REFERENCE: 27041P_WOAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: EP02 000 315.8 PRIOR FILING DATE: 2002-01-03
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CURRENT FILING DATE: 2003-01-03
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                                                         NUMBER OF SEQ ID NOS: 13
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Pred. No.
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ORGANISM: Artificial Sequence FEATURE:

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; ORGANISM: Homo sapiens
US-10-408-765A-1931
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US-10-291-265-332
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Best Local Similarity
Ches 6; Conserva
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PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 307
                                                     SEQ ID NO 1931
LENGTH: 311
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APPLICANT: Tang et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
                                                                                                                             CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
                                                                                                                                                               APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
                                                                                                                                                                                                                                                                      APPLICANT: Ghosh, Soumitra
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradfc
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PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
                                                                                        NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
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Taylor, Steven W.
Glenn, Gary M.
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US-10-612-783-4490
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                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4577_129850C.1.pep US-10-612-783-4490
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SEQ ID NO 334
LENGTH: 312
TYPE: PRT
                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: KA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53373)
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/612,783
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
SEQ ID NO 4490
LENGTH: 518
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Best Local (
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GENERAL INFORMATION
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CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR PRIOR DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
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nes 6; Conserv
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1 TGRIPP 6
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Pred. No.
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Pred. No.
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Pred. No. 10;
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US-10-408-765A-2802
                                                                                                    ; TYPE: PRT; ORGANISM: Homo sapiens US-10-286-897-3022
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US-10-286-897-3022
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US-10-408-765A-2802
Query Match
Best Local Similarity 83...
Stockers 5; Conservative
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Best Local Similarity bo...
Thes 5; Conservative
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SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 2802

LENGTH: 639
                                                                                                                                                         SOFTWARE: pt_FL_genes_b Versions 1.0
SEQ ID NO 3022
LENGTH: 334
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TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ghosh, Soumitre APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/99/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US/09/620,312
PRIOR FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/286,897
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
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                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 7143
                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/09/727,344 PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US/09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US/09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR FILING DATE: 2000-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/09/552,317
PRIOR FILING DATE: 2000-04-25
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83.3%;
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    Mismatches

                                              Score 30; DB Pred. No. 72;
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Pred. No.
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SEQ ID NO 3022
LENGTH: 334
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GENERAL INFORMATION:
APPLICANT: Hyseq In
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Best Local
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PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR FILING DATE: 2000-07-19
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                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/286,897
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
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PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
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PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US/09/653,450
PRIOR FILING DATE: 2000-08-31
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US/09/598,042
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7143
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PRIOR APPLICATION NUMBER: US/09/727,344 PRIOR FILING DATE: 2000-11-29
                                               PRIOR APPLICATION NUMBER: US/09/693,036 PRIOR FILING DATE: 2000-10-19
                                                                                   PRIOR APPLICATION NUMBER: US/09/662,191 PRIOR FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
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274 TGQIPP 279
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Pred. No.
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Mismatches
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Gaps

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CORRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR PPLICATION NUMBER: US/09/552,317
PRIOR APPLICATION NUMBER: US/09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US/09/653,450
PRIOR APPLICATION NUMBER: US/09/662,191
PRIOR APPLICATION NUMBER: US/09/662,191
PRIOR APPLICATION NUMBER: US/09/693,036
PRIOR APPLICATION NUMBER: US/09/693,036
PRIOR APPLICATION NUMBER: US/09/693,036
PRIOR APPLICATION NUMBER: US/09/797,344
PRIOR FILING DATE: 2000-11-2
PRIOR FILING DATE: 2000-11-2
SOFTWARE: PL_FL_genes_b Versions 1.0
SEQ ID NO 6594
LENGTH: 365
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-258-898A-6594
; Sequence 6594, Application US/10258898A
; GENERAL INFORMATION:
APPLICANT: Hyseq Inc
: TITLE OF INVENTION: NOVel Nucleic Acid and Polypeptides
; FILE REFERENCE: 704FLPCT
; CURRENT APPLICATION NUMBER: US/10/258,898A
; CURRENT FILLING DATE: 2002-10-29
; CURRENT FILLING DATE: 2002-10-29
Search completed: August 20, 2003, 12:45:15 Job time: 1.73494 secs
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; SEQ ID NO 6594
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-897-6594
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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305 TGQIPP 310
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Result
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Perfect score:
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score cand is
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protein search, using sw model
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1 TGRIPP 6
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T09356
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receptor protein k
brassinosteroid-in
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probable ATP synth
hypothetical prote
                  UDP galactose 4-ep
UDP-galactose 4-ep
alpha-1,2-N-acetyl
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           adenylate cyclase
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Om(2D) protein - f
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cylicin I - bovine
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                                                                                                                          probable receptor-
                                                                                                                                 Om(2D) protein
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μ,	3	_	hypothetical prote	conserved hypothet			_	hypothetical prote	salivary protein P	hypothetical prote	acetyl-CoA carboxy	L-CoA	acetyl-CoA carboxy	receptor-like prot	receptor-like prot

## ALIGNMENTS

acetoin catabolism protein Acox - Alcaligenes eutrophus (strain H16) C;Species: Alcaligenes eutrophus C;Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 30-Sep-1993 C;Accession: A42462

Schmidt,

B.; Steinbuechel,

of the Alcaligenes eutrophus

Ξ

RESULT A42462

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cylicin I - human (fragment)
c;Species: Homo sapiens (man)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change
C;Accession: B40713; S35920
R;Hess, H.; Heid, H.; Franke, W.W.
J. Cell Biol. 122, 1043-1052, 1993
A;Title: Molecular characterization of mammalian cylicin, a basi
A;Reference number: A40713; MUID:93359502; PMID:8354692
A;Status: preliminary
В
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B40713
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A:Title: Identification and molecular characterization (A:Reference number: A42462; MUID:91286190; PMID:2061286 A:Accession: A42462
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <PRID:
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                                                                                                               C; Keywords: cytoskeleton
                                                                                                                   A;Molecule type: mRNĀ
A;Residues: 1-598 <HES>
A;Cross-references: GB:Z22780; NID:g396104; PIDN:CAA80457.1; PID:g396105
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                                                                   Query Match
Best Local
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Best Local :
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544
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                         1 TGRIPP 6
                                                     Similarity
5; Conserv
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6; Conserv
TGRVPP 549
                                                      Conservative
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83.3%;
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45;
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                                                   Indels
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cylicin I - bovine
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change
C;Accession: A40713; S35913
R;Hess, H.; Heid, H.; Franke, W.W.
J. Cell Biol. 122, 1043-1052, W.J.
Cell Biol. 122, 1043-1052, 1993
A;Title: Molecular characterization of mammalian cylicin, a basi
A;Reference number: A40713; MUID:93359502; PMID:8354692
A;Accession: A40713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
SXAD97
                                                                                                                                                                                                                                                                                                                                         RESULT 5
SXAD93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 13, 375-385, 1981
A;Title: The gene for polypeptide IX of human adenovirus A;Reference number: A91480; MUID:81261948; PMID:6266923
A;Accession: A03854
A;Molecule type: DNA
A;Residues: 1-138 <DIJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: polypeptide IX
C;Species: Mastadenovirus h7 (human ade
C;Date: 18-Dec-1981 #sequence_revision
C;Accession: A03854
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C;Keywords: cytoskeleton
                                                                                                                                                                                                                                    hexon-associated protein (IX) - human adenovirus 3
C;Species: Mastadenovirus h3 (human adenovirus 3)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: B03854; A03854
R;Engler, J.A.
Gene 13, 387-394, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-138 <DIJ>
C; Superfamily: adenovirus hexon-associated protein
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A; Residues: 1-667 <HES>
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                                                                                                      C; Superfamil
C; Keywords:
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                                                                                                                    A;Cross-references: GB:J01962; NID:g209966; C;Superfamily: adenovirus hexon-associated
                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-138 <ENG>
                                                                                                                                                                                                     A; Title: The nucleotide sequence of the polypeptide IX A; Reference number: A91481; MUID:81261949; PMID:7262560
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                                                                                                      hexon-associated protein
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                                   Similarity 5; Conserv
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     TGRIPP
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83.3%;
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                                   Score 32; DB Pred. No. 15; Mismatches
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No.
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protein (IX)
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RyContains: FMN adenylyltransferase (EC 2.7.7.2); ribofiavin kinase (EC 2.7.7.2); c;Species: Neisseria meningitidis c;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001 C;Accession: A81982

RESULT A81982

R; Parkhill,

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Achtman,

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James,

K.D.;

Bentley,

S.D.;

Churcher,

C.; Klee,

. R.;

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l serogroup 2.7.1.26)

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regulatory protein nask - Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 04-Mar-2000
C;Accession: A55859
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                                                                                                                                                                                                                                                                                     R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Elsen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307
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Ъ
                               Qy
                                                                                                                                     A; Gene: NMB183
C; Superfamily:
                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-306 <TET>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: H81036
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A; Residues: 1-393 <GOL>
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A;Accession: A55859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 176, 5077-5085, 1994
A; Title: Identification and structure of
                                                                                                                                                                                        A; Experimental source: serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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5; Conserv
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   TGRMPP
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ce: serogroup B, strain MC58
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83.3%;
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83.3%;
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47;
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59;
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C;Accession: H71803

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human A; Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: H71803

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-613 <ARN>
                                                     A; Experimental source: C; Genetics:
                                                                                       A; Cross-references: GB: AE001568;
                                                                                                                                                                                                                                                                                  penicillin-binding protein - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb_1999 #sequence_revision 12-Feb-1999 #text_change 17-Mar-2000
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A;Note: it is uncertain whether Met-1 or Met-10 is the initiator
C;Superfamily: polygalacturanase-inhibiting protein; leucine-rich alpha-2-glycoprotein
F;274-297/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-342 < TOU>
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A;Title: Cloning and characterization of the gene encoding the A;Reference number: S23764; MUID:93272053; PMID:1303801

A;Accession: S23764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polygalacturanase-inhibiting protein precursor - kidney bean C;Species: Phaseolus vulgaris (kidney bean) C;Date: 05-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C;Accession: S23764
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C;Superfamily: conserv
C;Keywords: nucleotid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-318 < PAR>
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A;Accession: A81982
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5; Conserv
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5; Conser
             penicillin-binding
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83.3%;
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83.3%;
                                                                                     GB:AE001439;
             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
61;
                                                                                 NID:g4156083; PIDN:AAD07044.1;
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                                                                                                                                                                                                                                                Smith,
                                                                               PID:g41560
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                                                                             RESULT 13
C84527
probable receptor-like protein kinase [imported] - C;Specles: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-reb-2001 #sequence_revision 02-Feb-2001 C;Accession: C84527
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R; Yoshida, K.; L.
Genet.
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S51599
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A;Gene: FlyBase:Dana/Om(2D)
A;Cross-references: FlyBase:FBgn0010400
                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-671 < YOS>
A; Cross_references: EMBL: D26553;
                                                                                                                                                                                                                                                                                                                                                                                                                       Om(2D) protein - fruit fly (Drosophila ananassae) C;Species: Drosophila ananassae C;Date: 15-Jul-1995 #sequence_revision 01-Sep-199 C;Accession: S51599
                                                                                                                                                                                                                                                                                                                           A; Title: Retrotransposon-induced ectopic expression of the Om(2D) gene causes A; Reference number: S51599; MUID:95107256; PMID:7808408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Ittle: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: D64714
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                   A; Accession: S51599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKeson, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell division protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 17-Mar-2000
C;Accession: D64714
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A; Residues: 1-615 < TOM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 TGKIPP
                                                                                                                                                                                                                                                                                                                                                                      K.; Juni, N.; Awasaki, T.; Tsuriya, Y.; Shaya, Genet. 245, 577-587, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 TGKIPP 426
                                        1 TGRIPP
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                                                                                Similarity
5; Conserv
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TGKIPP 436
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5; Conserv
                                                                                  Conservative
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                                                                                                91.2%;
83.3%;
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83.3%;
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83.3%;
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                                                                            Score 31; DB
Pred. No. 1.46
1; Mismatches
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                                                                     DB 2; Lc..
1.4e+02;
~~ 0;
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1.3e+02;
0;
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                                                                                                                    Length 671
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Arabidopsis thaliana #text\_change 02-Feb-2001

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Jeuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999

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hypothetical protein T9N14.3 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C95745
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Cihi, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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A;Molecule type: DNA
A;Residues: 1-744 <STO>
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A; Gene: At2g15300
A; Map position: 2
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A;Reference number: 225262
A;Accession: T50851
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-981 <YAM>
                                                                                                                                   R;Yamamoto, E.; Karakaya, H.C.; Knap, H.T. Biochim. Biophys. Acta 1491, 333-340, 2000 A;Title: Molecular characterization of two
                                                                                                                                                                                                                                             receptor protein kinase homolog [imported] - soybean
C;Species: Glycine max (soybean)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
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A;Molecule type: DNA
A;Residues: 1-977 <STO>
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A;Accession: C96745
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255 TGKIPP 260
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83.3%;
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Pred. No.
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Pred. No. 2.1e+02;
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A;Cross-references: EMBL:AF197946; PIDN:AAF59905.1
C;Genetics:
A;Gene: CLV1A
                                                                                            C; Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology
 밁
                      οy
                                     Query Match
Best Local Similarity
"hes 5; Conserv
471 TGKIPP 476
                        1 TGRIPP 6
                                                 Conservative
                                                            91.2%;
83.3%;

    Mismatches

                                                                Pred.
                                                                          Score 31;
                                                                No.
                                                                           DB 2;
                                                              .1e+02;
                                                                          Length 981;
                                                     0;
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Search completed: August 20, 2003, 12:42:28 Job time: 6.19277 secs

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Result
No.
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HEX9_ADE077
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PGI2_PHAVU
PGI2_PHUMAN
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RBL2_MOUSE
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RBL2_HUMAN
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Q9h939 homo sapien
Q9eqn3 mus musculu
Q64700 mus musculu
P11029 gallus gall
Q9tts3 bos taurus
Q13085 homo sapien
Q28559 ovis aries
P02814 homo sapien
Q28559 ovis aries
P02814 homo sapien
Q99954 homo sapien
Q99954 homo sapien
Q99954 woodwardia
P59152 woodwardia
P59152 woodwardia
P59156 mecaca fasc
Q57891 methanococc
G57891 methanococcus
Q97196 chlamydla m
P59196 chlamydla m
P59196 chlamydla m
P59196 chlamydla m
P591844 schizosacch
Q00874 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P35663 homo sapien
P35662 bos taurus
P03283 human adeno
P52425 cuphea lanc
P5334 phaseolus v
P58822 phaseolus v
P58823 phaseolus v
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Q92643 homo sapien
P56881 thermus the
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streptomyce rickettsia	mus musculu turnip yell turnip yell drosophila	drosophila homo sapien mus musculu methanopyru escherichia

## ALIGNMENTS

RESULT GP18_H ID G AC Q DT 2 DT 2 DT 1 DT 1 DE G DE G	D dd	Be	DR KW SQ	88	888	388	88	88	88	RI.	R R	RA	굕 주 주	RP Ř	28	38	OS G	DE C	ij	DI AC	I ACO	RESULT
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TTTTREER REARES 
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RA Altachul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."

BT. Droc. Na+1 Assay Grim S. A 90-16890-16907200000
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Mammalia; Eutheria;
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PIGK OR GPI8.
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ACT_SITE
CONFLICT
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                                                                                            PRINTS; PR00776;
Hydrolase; Thiol
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                                                                                                                                                                                                               MEROPS; C13.005;
                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
lifted and this statement is not removed. Usage by an
ities requires a license agreement (See http://www.isb-
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.
PATHWAY: GPI-anchor biosynthesis.
SUBUNIT: Associates with PIGS and PIGT.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natl. Read. Sci. U.S.A. 99:16899-16903(2002).

C. Natl. Read. Sci. U.S.A. 99:16899-16903(2002).

FUNCTION: Mediates GPI anchoring in the endoplasmic reticulum, by replacing a protein's C-terminal GPI attachment signal peptide with a pre-assembled GPI. During this transamidation reaction, the GPI transamidase forms a carbonyl intermediate with the substrate
                                                                                                                                                                                                                                                  6050
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AF022913; AAB81597.1;
BC020737; AAH20737.1;
                                                                                                                                                     Pro; IPR001096; Legumain.
PF01650; Peptidase_C13; 1.
                                                                                                                                                                                                                                                                              HGNC:8965; PIGK
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etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9356492;
Tidenfriend S.,
                                                                                                                            HEMOGLOBNASE.
                                                                                               protease;
         164
206
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                                                                                                  GPI-anchor biosynthesis
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Best Local
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                                    InterPro; IPR002314; tRNA-synt_2
InterPro; IPR002320; tRNA-synt_t
InterPro; IPR006195; tRNA-ligase
pfam; PF03129; HGTP_anticodon; 1
Pfam; PF02824; TGS; 1.
Pfam; PF00587; tRNA-synt_2b; 1.
PRINTS; PR01047; TRNA-SYNTHTHR.
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30-MAY-2000
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 some structural and kinetic properties. Biochimie 76:71-77(1994).
-I- CATALYTIC ACTIVITY: ATP + L-threoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence analysis and modular organization of threonyl-tRNA synthetase from Thermus thermophilus and its interrelation with threonyl-tRNA synthetases of other origins.";
Eur. J. Biochem. 267:379-393(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Threonyl-tRNA
                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diphosphate + 1-threonyl-trna(Thr).
-!- COFACTOR: Binds 1 zinc ion per subunit.
-!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- DOMAIN: THE C-TERMINAL DOMAIN RECOGNIZES THE ANTICODON BASES.
-!- SIMILARITY: Belongs to class-II aminoacyl-trna synthetase fam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-45, AND CHARACTERIZ STRAIN-HB8 / ATCC 27634; MEDLINE-94304998; PubMed-8031907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-HB8 / ATCC 27634;
MEDLINE-20098514; PubMed-10632708;
                                                                                                                                                                                                                                                   EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehresmann C., Ehresmann B.;
"Threonyl-tRNA synthetase from Thermus
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Bacteria; Deinococcus-Thermus;
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; P00955; 1EV
P; MF_00184;
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Rel. 41, Last annotation
synthetase (EC 6.1.1.3)
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tRNA_ligase_II.
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RESULT 4
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Metal-binding; Zinc.
DOMAIN 234 548
DOMAIN 338 341
METAL 349 349
METAL 400 400
METAL 529 529
                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as modified and this statement is not removed. Us entities requires a license agreement (see http or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                         EMBL; Z22780;
PIR; B40713; I
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01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cylicin I (Multiple-band polypeptide I) (Fr.
CYLC1 OR CYL.1 OR CYL.
Homo sapiens (Human)
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                                                                                                                                                                                                                    Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- DEVELOPMENTAL STAGE: SPECIFIC TO LATE SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93359502; PubMed=8354692;
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Mammalla; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYL1_HUMAN
P35663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *Molecular characterization of mammalian cylicin, a basic protein the sperm head cytoskeleton.";
J. Cell Biol. 122:1043-1052(193).
1. FUNCTION: POSSIBLE ARCHITECTURAL ROLE DURING SPERMATOGENESIS.
BE INVOLVED IN SPERMATID DIFFERENTIATION.
1. SUBCELLULAR LOCATION: CALYX; SPERM HEAD CYTOSKELETAL STRUCTURE
1. TISSUE SPECIFICITY: Testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          less H., Held H., Franke W.W.;
                                                                                                                                                                                                                                 GO:0005856; C:cytoskeleton; NAS
GO:0005198; F:structural molecu
GO:0007283; P:spermatogenesis; I
                                                                                                                                                                                                                                                                                                    60312
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I) (Fragment).
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                                                                                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                    SEQUENCE
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REPEAT
                                                                                                                                                                      DOMAIN
                                                                                                                                                                              Cytoskeleton;
                                                                                                                                                                                       EMBL; Z22779; CAA80456.1; -. PIR; A40713; A40713.
                                                                                                                                                                                                                                                                                   -1- DEVELOPMENTAL STAGE: SPECIFIC TO LATE SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOVIN
                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-JUN-1994 (Rel.
01-NOV-1997 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93359502;
                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Testis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P35662;
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613
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                1 TGRIPP 6
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TGRVPP
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5; Conserv
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94 (Rel. 29, Last sequence update)
97 (Rel. 35, Last annotation updat
(Multiple-band polypeptide I).
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517
548
617
667
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Franke W.W.;
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305
337
368
405
442
516
569
                                                                    74817 MW;
                                        97.1%;
83.3%;
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83.3%;
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Pred. No.
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                                                                 PRO-RICH.
CBF66EA462243D91 CRC64;
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Pred. No.
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                                 Mismatches
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ed. No. 18;
Mismatches
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; I).
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                                        20;
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RESULT

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RESULT 7
GPDA_C
GPDA_C
AC P52425
DT 01-0CT
DT 15-JUL
DE Glycer
GN GPDH.
OS Cuphea
OC Eukary
OC Sperma
OC MCBL_T
RN [1]
RP SEQUEN
RA Hausma
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Best Local S
Matches 5
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P03283;
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21-JUL-1986
15-DEC-1998
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                                                                                                                      P52425;
01-OCT-1996
01-OCT-1996
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-Human adenovirus type 7; STRAI MEDLINE-81261948; PubMed-5266923; Dijkema R., Maat J., Dekker B.M.M., va"The gene for polypeptide IX of human Gene 13:375-385(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The nucleotide sequence adenovirus type 3."; Gene 13:387-394(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human adenovirus type
Human adenovirus type
                               Spermatophyta; Magnoliophyta; enbryophyta; Epermatophyta; Magnoliophyta; eudicotyledons; core eu eurosids II; Myrtales; Lythraceae; Cuphea.
NCBI_TaxID=3930;
                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
Glycerol-3-phosphate dehydrogenase [NAD+] (
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or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hexon-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
   Hausmann L.,
                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content ified and this statement is not removed. Usage by and ities requires a license agreement (See http://www.isb-send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: THIS PROTEIN IS A STRUCTURAL COMPONENT OF THE VIRIO MAY HAVE AN ADDITIONAL ROLE DURING ADENOVIRUS MULTIPLICATION.
                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                              TGRIPP
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(Rel.
(Rel.
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     Schell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenovirus type 3;
949; PubMed=7262560;
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. 37, Last annotation update)
protein (Protein IX).
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37,
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the polypeptide IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA stage;
                                                                                                                                                                                                                                                                               score 32; DB; Pred. No. 6.3; 1; Mismatches
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     ₽.
                                                                                                            ion update) [NAD+] (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     van Ormondt H., Boyer H.W.;
an adenovirus type 7.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adenovirus type
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                                                                n; Tracheophyta;
eudicots; Rosid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning of a CDNA coding for a glyc
from Cuphea lanceolata";
(In) Kader J.-C., Mazliak P. (eds.);
Plant lipid metabolism, pp.534-536,
Dordrecht (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _PHAVU
                                                                                                                                                                                                                                                                       phaseolus vulgaris (Kidney bean) (French bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoldeae; Phaseoleae; Phaseolus.
NCBI_TaxID=3885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006168; NAD_Gly3P_dh.
InterPro; IPR006109; NAD_Gly3P_dom.
Pfam; PF01210; NAD_Gly3P_dh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- CATALYTIC ACTIVITY: Sn-glycerol 3-r
phosphate + NADH.
-i- SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                    PGIP1
                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel.
01-JUN-1994 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X79677; CAA56125.1;
                                                                                                                                                        Toubart P., Desiderio A., Salvi G., Cervone F., Daroda L de Lorenzo G., Bergmann C., Darvill A.G., Albersheim P., "Cloning and characterization of the gene encoding the endopolygalacturonase inhibiting protein (PGIP) of Phase
 Leckie F., Mattei B., Capodicasa C., Hemmings A., Nuss L. De Lorenzo G., Cervone F.; De Lorenzo G., Cervone F.; "The specificity of polygalacturonase-inhibiting protein single amino acid substitution in the solvent-exposed beta-strand/beta-turn region of the leucine-rich repeats
                                                                  SEQUENCE FROM N.A., AND MUTAGENESIS STRAIN-CV. Pinto; TISSUE-Hypocotyl; MEDLINE-99246261; PubMed-10228150;
                                                                                                                                                                                                                 STRAIN=cv. Saxa; TISSUE=Hypocotyl;
MEDLINE=93272053; PubMed=1303801;
                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               protein) (PGIP-1).
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P35334;
                                                                                                                               Plant J.
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                                                                                                                                 2:367-373(1992).
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29, Last sequence update)
41, Last annotation update)
inhibitor 1 precursor (Poly
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83.3%;
region
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18;
                                                                                                       LYS-253
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ENT GLYCEROL-3-PHOSPHATE
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Phaseolus
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Best Local S
Matches 5
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EMBL; A23205; CAA01664.1; -
PIR; S23764; S23764.
InterPro: IPR001611; LRR.
InterPro: IPR007090; LRR_pl
Pfam; PF00560; LRR; 4.
 PGI2_PHAVU
P58822;
28-FEB-2003
28-FEB-2003
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                                   PHAVU
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CARBOHYD
MUTAGEN
                                                                                                                                                                                                                                                                                      Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specificities are expressed in Phaseolus vulgaris.";
Mol. Plant Microbe Interact. 10:852-860(1997).

-I- FUNCTION: Inhibitor of fungal polygalacturonase. It is an important factor for plant resistance to phytopathogenic fungi. Substrate preference is polygalacturonase (PG) from A.niger >> of F.oxysporum, A.solani or B.cinerea. Not active on PG from F.monlilforme.
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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REPEAT
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Van Roekel J.S., Baulcombe D.C.,
Cervone F.;
                                                                                                                                        SEQUENCE
                                                                                                                                                                         CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97449843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Cell-wall associated MISCELLANEOUS: Mutation of Lys-253 confers the F.moniliforme PG. SIMILARITY: BELONGS TO THE POLYGALACTURONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY:
                                                                      216
                                                                                                     Similarity
5; Conserv
                                                                                                                                                                                                                                                                                              Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a new recognition capability.";
18:2352-2363(1999).
                                                                      TGKIPP
                                                                                    TGRIPP 6
 (Rel. 41, Rel. 41,
                                                                                                                                                                                                                  129
153
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                                                                                                      Conservative
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Aracri B., Leckie F.,
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                          STANDARD;
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83.3%;
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 sequence, update)
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NKED (GLCNAC...) (PO
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BROADER SPECTRUM OF
0F94E0D2A39598 CRC64;
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t-1 or Met-10 is the
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                                                                               MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           De Lorenzo G., Cervone F.;
"The specificity of polygalacturonase-inhibiting protein (PGIP) single amino acid substitution in the solvent-exposed beta-strand/beta-turn region of the leucine-rich repeats (LRRs) confers a new recognition capability.";
EMBO J. 18:2352-2363(1999).
  MUTAGEN
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SIGNAL
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MEDLINE-99246261;
                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007090;
Pfam; PF00560; LRR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein) (PGIP-2)
PGIP2.
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lda M.S., Feder1~
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H->Q: NO EFFECT.
Q->K: NO EFFECT;
A->S: NO EFFECT;
ASSOCIATED WITH G
WHEN ASSOCIATED W
A->S: NO EFFECT.
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Papilionoideae; Phaseoleae; Phaseolus.
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                                                                                                                                                            70% DECREASE
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H K-253;
H S-326.
                  G-181; LOSS OF WITH K-253.
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                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- TISSUE SPECIFICITY: Found in suspension-cultured lesser extent in hypocotyls, leaves and flowers.
-i- SIMILARITY: BELONGS TO THE POLYGALACTURONASE-INHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toubart P., Desiderio A., Salvi G., Cervone F., Daroda L., de Lorenzo G., Bergmann C., Darvill A.G., Albersheim P.; de Lorenzo and characterization of the gene encoding the "Cloning and characterization of the gene encoding the endopolygalacturonase-inhibiting protein (PGIP) of Phaseolus vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-cv. Pinto; TISSUE-Hypocotyl; MEDLINE-93272053; PubMed-1303801;
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PGIP3.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Polygalacturonase inhibitor 3 precursor (Poly
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ain; Cell wall; !
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LRR 7.

BY SIMILARITY.

BY SIMILARITY.
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                                    Pred. No. 27;
l; Mismatches
                                                                      Score 31;
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eudicotyledons; core eudicots; Rosid
; Papilionoideae; Phaseoleae; Phaseol
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RESULT 11
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
BRASSINOSTEROID INSENSITIVE 1 precursor (EC 2.7.1.37) (AtBRIL)
(Brassinosteroid LRR receptor kinase).
BRII OR AT4G39400 OR F23K16.30.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; core eudicots; Rosid;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid;
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STRAIN-cv. Columbia;
MEDLINE-203000000
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"A putative leucine-rich repeat recebrassinosteroid signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Muel Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20083488; PubMed=10617198;
Mayer K.F.X., Schueller C., Wambutt R.,
Pohl T., Duesterhoeft A., Stiekema W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Friedrichsen D.M., Joazeiro C.A.P., Li J., Hunter "BRASSINOSTEROID-INSENSITIVE-1 is a ubiquitously rich repeat receptor serine/threonine kinase."; Plant Physiol. 123:1247-1256(2000).
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MEDLINE=97442355; PubMed=9298904;
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BRI1-104; BRI1-113 AND
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Feldmann K.A., Tax F
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AND BRI1-115.
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RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S., RA Chefdor F. Cooke R., Berger C., Monfort A., Casacuberta E., Ra Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E., Ra Chefdor F., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Pernet P., Wandenbol M., Bargues M., Terol J., Torres A., Ra Perpez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T., Ra Perper S., Schwarz S., Scholler P., Heber S., Tacon D., Jesse T., Ra P., Bent P., Bevan M., Milson R.K., de la Bastide M., Habermann K., Ra Zaccaria P., Bevan M., Milson R.K., de la Bastide M., Habermann K., Ra Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., Ra Schon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., Ra Schonking T., Kalicki J., Graves T., Harmon G., Edwards J., Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Ra Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J., Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Ra Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., Ra K., Bentley D., Rardis E., Dante M., Pepin K., Hillier L., Ra Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Ra Antonolu B., 2idanic M., Strong C., Sun H., Lamar B., Yordan C., Ra Antonolu B., 2idanic M., Strong C., Sun H., Lamar B., Yordan C., Ra Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Ra Swaby I. K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Ra Chen E., Marra M., Martienssen R., McCombie W.R.; Thaliana.", Martiensen R., McCombie W.R.;
Lid., Wen J., Lease K.A., Doke J.T., Tax F.E., Walker J.C.;

"BAK1, an Arabidopsis LRR receptor-like protein kinase, interacts with BRII and modulates brassinosteroid signaling.";

Cell 110:213-22(2002).

-1- FUNCTION: Receptor with a serine/threonine-protein kinase activity. Regulates, in response to brassinosteroid binding, a signaling cascade involved in plant development, including expression of light- and stress-regulated genes, promotion of cell elongation, normal leaf and chloroplast senescence, and flowering. Binds brassinolide, and less effectively castasterone, but not 1,3/22,3-0-textramethylbrassinolide or ecdysone. May be involved in a feedback regulation of brassinosteroid biosynthesis.

--- CATALTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

--- SUBUNIT: Heterodimer with BAK1.

--- SUBURIT: Heterodimer with BAK1.
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MEDLINE-20336852; PubMed-10875920;

He Z., Wang Z.-Y., Li J., Zhu Q., L.

"Perception of brassinosteroids by
receptor kinase BRI1.";
Science 288:2360-2363(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20484044; PubMed-11027724; Oh M.-H., Ray W.K., Huber S.C., Asara J.M., Gage D.A., Cl "Recombinant BRASSINOSTEROID INSENSITIVE I receptor-like autophosphorylates on serine and threonine residues and phosphorylates a conserved peptide motif in vitro."; Plant Physiol. 124:751-768(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION, AND INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell 110:203-212(2002).
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extracellular domain of the
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receptor for plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinase
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RESULT 12
PSP2_HUMAN
ID PSP2_HUMAN
AC Q9H939;
                                                                                                                                       밁
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                                                                                                                                                                                                                                                                                                                    Matches
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Query Match
Best Local
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InterPro; IPR007090; LRI
InterPro; IPR000719; pro
InterPro; IPR002290; Sei
InterPro; IPR001245; Typ
Pfam; PF00560; LRR; 17;
                                                                                                                                                     REPEAT
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EMBL; AL078620; CAB44
EMBL; AL161595; CAB80
PIR; T09356; T09356.
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase; 1.
PRINTS; PR00019; LEURICHRPT.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                   Leucine-rich
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                               Transferase; Kinase; Serine/threonine-protein kinase; Recept Steroid-binding; ATP-binding; Repeat; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: A 70 amino acid island between the 20th and the 21th LRR is essential for the binding of brassinosteroids.

MISCELLANEOUS: Binding of brassinosteroid induces intramolecular autophosphorylation of BRII. Interaction with BAKI activates both receptor kinases and the full activation of either receptor kinases requires transphosphorylation by their partners. Optimum in vitro phosphorylation of the substrate requires Arg or Lys residues at P-3, P-4, and P+5 (relative to the phosphorylated amino acid at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Expressed ubiquitously.
DEVELOPMENTAL STAGE: Expressed constitutively
light-grown seeddlings.
DOMAIN: Contains one leucine-zipper motif and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: Phosphorylated on at least 12
  429
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                                    \vdash
                                                                       Similarity
5; Conserv
TGKIPP 434
                                    TGRIPP 6
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                   repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES Contains 25 leucine-rich (LRR) repeats.
                                                                                                                                                     1196
813
121
146
169
197
221
221
268
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; Prot_kinase.
; Ser_thr_pkinase.
                                                                                        91.2%;
83.3%;
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Cys (Cys pair 1 and
                                                                 Score 31; DB
Pred. No. 1e+0
1; Mismatches
                                                                                                                                             POTENTIAL.
LRR 1.
LRR 2.
LRR 3.
LRR 4.
LRR 5.
LRR 6.
LRR 6.
LRR 7.
LRR 8.
                                                                                                                                                                                                                                                                                                                          BRASSINOSTEROID
                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                             Phosphorylation
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                                                                                                          DB 1;
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,
A Hong L., Sonetz N.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Roman S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.W.,
A Willalon D.K., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length
A human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., "NEDO human cDNA sequencing project.", "NEDO human cDNA sequencing project.", "NEDO human cDNA sequencing project.", submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Binds to Fractin. May be involved in regulation of the actin cytoskeleton (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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28-FEB-2003 (Rel.
15-SEP-2003 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                EMBL; AK023100; BAB14404.1;
EMBL; BC035395; AAH35395.1;
Genew; HGNC:9581; PSTPIP2.
                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
PROSITE;
                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: Phosphorylated on tyrosine (B
SIMILARITY: Contains 1 FCH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note=No experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9H939-2; Sequence=VSP_004070;
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41,
42,
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Last sequence update)
Last annotation update)
ine phosphatase-interacting protein
                                                                                                                          Cdc15_Fes_CIP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     confirmation available;
tyrosine (By similarity).
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RESULT 13
TIZ2_MOUSE
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Best Local
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                                                       Query Match
Best Local
                                              Matches
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DOMAIN
DOMAIN
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16-OCT-2001 (R
TSC22-related
                                                                                                                                                                                                                                                                                                                                                     "Identification: "Identification: "Identification: genes related to TSC22.";
genes related to TSC22.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: TRANSCRIPTIONAL REPRESSOR (BY SIMILARITY).
-I- FUNCTION: TRANSCRIPTIONAL REPRESSOR (CAN FORM AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9EQN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                             Pfam; PF01166; TSC22; 1.
ProDom; PD007152; TSC-22_Dip_Bun; 1.
PROSITE; PS01289; TSC22; 1.
                                                                                                                                                                             HSSP; P80220; 1DIP.
MGD; MGI:1926079; 0610009M14Rik.
                                                                                                                                                                                                                           or send
                                                                                                                                                                                                                                     entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                         "Identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6-0CT-2001
                                                                                                                  Transcription
                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear (Potential). SIMILARITY: BELONGS TO THE TSC-22/DIP/BUN FAMILY.
                                                                                                                                                                                                                                                                                                                                               SUBUNIT: FORMS HOMODIMER OR WITH TSC-22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
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 246 TGKVPP 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 5; Conserv
                                                                                                                                                                                                                             an email to license@isb-sib.ch).
                                              Similarity 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGRIPP
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                         TGRIPP 6
                                                                                                                                                                  IPR000580;
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
ed inducible leucine zipper protein
                                                                                              387
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                                               Conservative
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                                                                                                          regulation; Repressor; Nuclear 357 LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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39987 MW;
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Pred. No.
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MYEQVERKSLEMCSIQROLEYEVNORKTGQIPPAPIMHENFY
SSQKNAVPAGKATGPULARRGELPIFKSSPDDPNYSLVDDY
SLLVQ -> HPSCMRISTPPRRMQSQQERLQGLTWQGEDPS
QFLKAHQMIPITLWLMTTVCSISKINETRAFSG (in
                                                2
                                                           Score 30;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0A8C9FD4C419A2B8 CRC64;
                                                                                               C78BB96B5B2DFB90 CRC64;
                                                ore 30; DB ed. No. 50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         J.W.M.;
of a far
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 AA
                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
43;
                                                                                                                                                                                                                                                                                                                                                                                                           family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                        1;
                                                                                                                      protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 333
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                                                                          Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                              of leucine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinae;
                                                                                                                                                                                                                                                                              restrictions on
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                                                                                                                                                                                                                                                                                                                                                                 HETERODIMER
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                                                                                                                                                                                                                                                                                              collaboration
                                                                                                                                                                                                                                                                                             outstation
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                                                   Gaps
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RESULT

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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

REQUIRE—96203998; PubMed—8622859;

RA Lecouter J.E., Whyte P.F.M., Rudnicki M.A.;

RA Lecouter J.E., Whyte P.F.M., Rudnicki M.A.;

RT "Cloning and expression of the Rb-related mouse pl30 mRNA.";

CC "I- FUNCTION: MAY HAVE A FUNCTION IN CELL CYCLE REGULATION. BINDS TO CC AND MAY BE INVOLVED IN THE TRANSFORMING CAPACITY OF THE ADENOVIRUS CC E1A PROTEIN. MAY ACT AS A TUMOR SUPPRESSOR. POTENT INHIBITOR OF CC E2F-MEDIATED TRANS-ACTIVATION, ASSOCIATES. PREFERENTIALLY WITH CC E2F-MEDIATED TRANS-CCITVATION, ASSOCIATES. PREFERENTIALLY WITH CC E2F5. BINDS TO CYCLINS A AND E (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- PTM: Phosphorylation on Ser-669 in G1 leads to its ubiquitin-

Ammendent proteolysis (By similarity).
                                     DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RBL2_MOUSE
Q64700;
30-MAY-2000
                                                                                                                                         Phosphorylation; Anti-oncogene
DOMAIN 414 1021 Pr
                                                                                                                                                                                                                                                                                                   MGD; MGI:105085; Rb12.
InterPro; IPR006670; Cycli;
InterPro; IPR002720; RB_A.
InterPro; IPR002719; RB_B.
                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T02972; MGD; MGI:105085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDILINE-96.199216; PubMed-8621630;
Chen G., Guy C.T., Chen H.W., Hu N., Lee E.Y.H.P.,

Molecular cloning and developmental expression of
member of the retinoblastoma gene family.";

J., Biol. Chem. 271:9567-9572(1996).
                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning, expression, and developmental characterization the murine retinoblastoma-related gene kb2/p130."; Cell Growth Differ. 6:1659-1664(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Retinoblastoma-like protein 2 (130 kDa
protein) (PRB2) (P130) (RBR-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pertile P., Baldi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                      PF01858; RB_A; 1.
PF01857; RB_B; 1.
; SM0385; CYCLIN; 2.
cription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                             U36799; AAB48991.1; -. U50850; AAC52598.1; -. U47333; AAC52555.1; -. P06400; IGUX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=9019172;
A., de Luca A.,
                                                                                                                                                                                                                                                                                                                                                             Cyclin.
POCKET (BINDS E1A).
DOMAIN A.
SPACER.
DOMAIN B.
POLY-PRO.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virgilio L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kDa retinoblastoma-associated
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р130,
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RESULT 15
COAC_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 5
                                                                                                                    acetyl-CoA carboxylase.";
FEBS Lett. 212:98-102(1987).

-I- FUNCTION: CATALYZES THE RATE-LIMITING REACTION IN THE BIOGENESIS
OF LONG-CHAIN FATTY ACIDS. THIS PROTEIN CARRIES THREE FUNCTIONS:
BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE, AND
                                                               -!- CATALYTIC ACTIVITY:
- ADP + phosphate +
-!- COFACTOR: BIOTIN.
                                                                                                         CARBOXYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) [Incarboxylase (EC 6.3.4.14)]
                                                                                                                                                                                Takai T., Wada K., Tanabe T.;
"Primary structure of the biotin-binding site of
                                                                                                                                                                                                         MEDLINE-87106011; PubMed-2879745;
                                                                                                                                                                                                                                SEQUENCE OF 493-820 FROM N.A.
                                                                                                                                                                                                                                                                   Takai T., Yokoyama C., Wada K., Tane "Primary structure of chicken liver from cDNA sequence.";
                                                                                                                                                                                                                                                                                                MEDLINE-88139305; PubMed-2893793;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Archosauria; Aves; Neogn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                     from cDNA sequence.";
J. Biol. Chem. 263:2651-2657(1988).
                                                                                                                                                                                                                                                                                                               TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
     SUBCELLULAR LOCATION: Cytoplasmic SIMILARITY: PARTIAL TO CARBAMOYL I
                                     ENZYME REGULATION: BY PHOSPHORYLATION. PATHWAY: Long-chain fatty acid biosynthesis;
                                                                                                + malonyl-CoA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     691 SGRIPP 696
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                   ; Chordata;
Neognathae;
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83.3%;
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                                                                                                         ATP +
                                                                       carboxybiotin-carboxyl-carrier
                                                                                   ATP +
     CARBAMOYL PHOSPHATE SYNTHETASES
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POLY-GLU.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
MISSING (IN REF. 3).
A -> P (IN REF. 2).
A -> P (IN REF. 1).
C -> S (IN REF. 1).
S -> T (IN REF. 1).
C -> R (IN REF. 2).
A -> P (IN REF. 1).
C -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥ε,
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A -> R (IN REF. 1)
P -> A (IN REF. 3)
PT -> RA (IN REF.
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Pred. No. 1.6e+02;
1; Mismatches 0
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                                                                                  biotin-carboxyl-carrier
                                                                                                      acetyl-CoA + HCO(3)(-) - ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ν̈́
                                                                                                                                                                                                                                                                                      Tanabe T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0565E4F998ACCAOD CRC64;
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I (IN REF. 1
                                                                                                                                                                                                                                                                          acetyl-CoA carboxylase deduced
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                                     first (rate-limiting)
                                                                                                                                                                                     chicken
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                                                                                  protein
                                                                      protein.
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SO THE TENT WENT TO DE REPORT TO THE TENT OF THE TENT 
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DR InterPro; IPR005482; Biotin_lipoyl.

DR InterPro; IPR000089; Biotin_lipoyl.

DR InterPro; IPR000089; Carboxyl_trans.

DR InterPro; IPR000012; Carboxyl_trans.

DR InterPro; IPR005481; CPase_L_N.

DR Pfam; PF00785; Biotin_carb_C; 1.

DR Pfam; PF00784; biotin_lipoyl; 1.

DR Pfam; PF00789; CPSase_L_Chain; 1.

DR Pfam; PF00789; CPSase_L_Chain; 1.

DR Pfam; PF00786; CPSase_L_D2; 1.

DR Pfam; PF00786; CPSase_L_D2; 1.

DR PROSITE; PS00188; BIOTIN; 1.

DR PROSITE; PS00186; CPSASE_1; 1.

DR PROSITE; PS00867; CPSASE_2; 1.

R PROSITE; PS00867; CPSASE_2; 1.

R PROSITE; PS00867; CPSASE_3; Biotin; Ligase; Multifunctional enzyme;

W ATP-binding; Phosphorylation.

The Property of the
Search completed: August 20, 2003, 12:35:02 Job time: 3.38822 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 5
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EMBL; X05019; CAA28675.1; -.
PIR; A29924; A29924.
HSSP; P24182; IDV1.
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                                                                                                                                                                                                                                                 907 SGRIPP 912
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5; Conservative
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441
786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
BY SIMILARITY.
BIOTIN.
BHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
COENZYME A-BINNING (BY SIMILARITY).
7 MM; 3F1C541F01BBBEF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 1; Length 23; Pred. No. 3.3e+02; Indels 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2324;
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Result
No.
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Perfect score:
Sequence:
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   111111 987654321
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length:
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1: sp_archea:*
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34
1 TGRIPP 6
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sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
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Q9LKZ6
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                            Q9LKZ4
Q8LHW9
Q92KC5
Q8BXX3
Q8BH63
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Q8BL63
Q8RU53
Q8L4U4
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        Q8ezu7 leptospira
Q9vnu2 drosophila
Q33417 pseudomonas
Q82432 malus domes
Q91kz6 glycine max
Q91kz6 glycine max
Q91kz6 yoryza sativ
Q92kc5 rhizobium m
Q8bx3 mus musculu
Q8bh63 mus musculu
Q8h7t3 oryza sativ
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Q8EZU7
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Best Local Similarity
Matches 6; Conserv
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# ALIGNMENTS

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RESULT
Q9VNU2
ID Q9
AC Q9
DT 01
DT 01
DT 01
DT CC
GN CC
Q9VNU2 PRELIMINARY;
Q9VNU2;
01-MAY-2000 (TrEMBLrel. 13, 0
01-MAY-2000 (TrEMBLrel. 13, 1
01-MAR-2003 (TrEMBLrel. 23, 1
CG11440 protein (HL01743p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
signal peptidase I (EC 3.4.21.89).
SIPC OR LA3754.
                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE011531; AAN50952.1; -. Hydrolase; Complete proteome. SEQUENCE 198 AA; 22758 MW; 5D8B8F7351B65237 CRC64;
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STRAIN-56801 / Serogroup Icterohaemorrhagiae / Serovar lai;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Spirochaetes;
NCBI_TaxID=173;
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                            Created)
Last sequence update)
Last annotation update)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                          Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S. Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                Submitted (JUN-2002) to the EMBL; AE003597; AAF51828.1; EMBL; AY119567; AAM50221.1;
                                                                                                                                                                 Patel S., Ph
Celniker S.;
                                                                                                                      FlyBase; FBgn0037163; CG11440.
                                                                                                                                                                                                                                   STRAIN=Berkeley;
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                                                                                                          InterPro; IPR000326; PA_PTPase.
                                                     госат
                                                                 Match
 231 TGRIPP
                                                                                                PF01569;
                                          Similarity 6; Conserv
                     TGRIPP
                                          Conservative
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                                          Score 34; DB Pred. No. 46; Mismatches
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V., Park S.,
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01-JAN-1998
01-DEC-2001
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01-NOV-1998 (
01-NOV-1998 (
01-MAR-2003 (
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Pfam; PF0
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                                                                                                                                       "A leucine-rich repeat receptor-like protein kinase induced in Malus x domestica by Venturia inaequalis salicylic acid treatment."; plant Mol. Biol. 40:945-957(1999).
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                                                                                                                                                                                                                                                                                                                                                                                               Malus domestica (Apple) (Malus sylvestris).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa PAO during cloning of the arylsulfatase gene cur. J. Biochem. 229:385-394(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATSB
  InterPro;
InterPro;
                                                            EMBL; AF053127; AAC3
InterPro; IPR001611;
InterPro; IPR007090;
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                                                                                                     -!- SIMILARITY: BELONGS TO EMBL; AF053127; AAC36318.1;
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                                                                                                                                                                                                                                                   MEDLINE=99454543; PubMed=10527419; Komjanc M., Festi S., Rizzotti L.,
                                                                                                                                                                                                                                                                                              STRAIN-CV.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3750;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purification and characterization of the arylsulfatase synthesized
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Bacteria; Proteobacteria;
Pseudomonadaceae; Pseudomo
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                                           InterPro;
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Z48540; CAA88423.1; -
Pro; IPRO00515; BPD_transp.
PF00528; BPD_transp.
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001 (TrEMBLrel. 19, Last annotation update)
transporter, putative membrane subunit.
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  IPR002290;
IPR001245;
                                        IPR000719;
                                                                                                                                                                                                                                                                                              Florina;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TIEMBLrel. 08, Created)
(TIEMBLrel. 08, Last sequence update)
(TIEMBLrel. 23, Last annotation update)
h receptor-like protein kinase.
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Prot_kinase.
Ser_thr_pkinase.
Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                            LRR_plant
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19,
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                                                                                                                          SER/THR
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                                                                                                                               PROTEIN KINASES
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infection
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Best Loc
Matches
                                                                                                                                                                                                                                              Query Match
Best Local
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**Nol. Biol. Evol. 18:1522-1531(2001).

-i- SIMILARTYY: BELONGS TO THE SER/THR FAMILY OF EMBL; AF244888; AAF91322.1; -

InterPro: IPRO01611; LRR.

InterPro: IPR007999; LRR_plant.

InterPro: IPR004838; NHtransf.1.

InterPro: IPR000719; Prot_kinase.

InterPro: IPR002290; Ser_thr_pkinase.

InterPro: IPR006023; In_MTpeptdse.
                                                                                                                                                                                                                    Matches
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PRINTS; PRO0109; TYRKINASE.

PRODOM; PRO0101; PROTEIN_KINASE; 1.

PROSITE; PS00107; PROTEIN_KINASE_DOM; 1

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Receptor; Serine/th
                                                                                                                                                                                                                                                                                                                                             Pfam; PF00560; LRR; 19.

Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Prot_kinase; 1.

PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.

PROSITE; PS50502; LRR_PS; 6.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9LKZ6 PRELIMINARY;
Q9LKZ6;
01-OCT-2000 (TrEMBLrel. 15, Cr.
01-OCT-2000 (TrEMBLrel. 15, La.
01-MAR-2003 (TrEMBLrel. 23, La.
Receptor-like protein kinase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-21363855; Yamamoto E., Knap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Glycine CEI_TaxID-3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a gene family.
Mol. Biol. Evo
-!- SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                          484
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                                                                                                                                                                                                                  Similarity
6; Conserv
                                                                                                          TGRIPP
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                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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pkinase;
                                                                                                          489
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H.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110101 MW;
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                                                                                                                                                                                                                                                                                                                      Serine/threonine-protein kinase; Transferase 109724 MW; 4C803E0F913C59E5 CRC64;
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Pred. No. 1.4
); Mismatches
                                                                                                                                                                                                            Score 34; DB Lv;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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annotation update)
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                                                                                                                                                                                                                                                                 Length 1008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  divergence
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                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT OR CHAPTER OF THE COLOR OF THE CASE OF THE CASE
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Best Local S
Matches
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InterPro; IPR006025; Zn_MTpeptdse.
Pfam; PF00560; LRR; 19.
Pfam; PF00560; LRR; 19.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00019; LEURICHRET.
PRINTS; PR00019; TYRKINASE; 1.
PRODOM; PD000001; PYOT_kinase; 1.
PROSITE; PS05001; PROTEIN_KINASE_DOM; 1.
PROSITE; PS050101; PROTEIN_KINASE_ST; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
ATP-binding; Kinase; Serine/thronine_prosites.
                                             STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto
"Oryza sativa nipponbare(GA3) genc
clone:P0022B05.";
Submitted (OCT-2001) to the EMBL/C
EMBL; AP004262; BAC10827.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8LHW9;
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLK3
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Q9LKZ4;
                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Etreptophyta; Et
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical P0022B05.33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3847;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001611; LRR.
InterPro; IPR007090; LRR_
InterPro; IPR000719; Prot
InterPro; IPR002290; Ser_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF244890; AAF91324.1; HSSP; P12931; 1FMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a gene family.";
Mol. Biol. Evol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine max (Soybean)
                              Gramene;
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6MHT80
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"Soybean receptor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor-like
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Evol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
6; Conserv
                              Q8LHW9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGRIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGRIPP
  IPR001611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1012
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Llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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  LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prot_kinase.
Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine/threonine-protein kinase; Tr
110322 MW; FD555FB57F99815D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRR_plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            22,
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Last
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Last sequence u
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB
Pred. No. 1.4
D; Mismatches
                                                                                                                              moto K.;
genomic
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Q1-DEC-2001 (TrEMBLrel. 19, C
Q1-DEC-2001 (TrEMBLrel. 19, I
Q1-MAR-2002 (TrEMBLrel. 20, I
Hypothetical protein R01632
R01632 OR SMCQ0940.
             Q8BXX3;
01-MAR-2003
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GPI transami
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Rhizobiaceae; Sinorhizobium
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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musculus
               transamidase homolog
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Pred. No.
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Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
[1]
                                                                                                                                                                                                                                                                   the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome b 60,770 full-length cDNAs ";
Nature 420:563-573(2002).
EMBL; AK077893; BAC37051.1;
EMBL; AK072806; BAC37051.1;
SEQUENCE 395 AA; 44895 MW; 4765ADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome k 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
REMBL, AK043033; BAC31442.1; -.
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01-MAR-2003 (TrEMBLrel.
Putative SKP1-like prote
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Mammalia; Eutheria;
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STRAIN-Nipponbare;

MCCombie W.R., de la Bastide M., Spiegel L., Preston R., Kirchoff K., MCCombie W.R., de la Bastide M., Santos L., Zutavern T., Miller B., Kuit K., Nascimento L., Baker J., Santos L., Zutavern T., Miller B., Cunnius D.M., Katzenberger F., Muller S., Bell M., Balija V., Shah R. King L., Yang C., Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;

"Genomic sequence for Oryza sativa, Nipponbare strain, clone

"Genomic sequence for Oryza sativa, Nipponbare strain, clone
                                                                                                                                                                                                                                                                                                                                          QBRU53;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
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Q8BL63;
Q1-MAR-2003
Q1-MAR-2003
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                                                                                                                                                                                                           Oryza sativa (Rice).

Gukaryota; Viridiplantae; Str.

Spermatophyta; Magnoliophyta;

Ehrhartoldeae; Oryzeae; Oryza

NCBI_TaxID-4530;
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Wing R.A.,
Currie J.,
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Nature 420.563-573(2002).
EMBL; AK046246; BAC32653.1; -
SEQUENCE 442 AA; 49784 MW; 0A907F7
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AC107224; AAN60492.1; -.
SEQUENCE 423 AA; 47756 MW; 2DE1454ACA8C643E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6J; TISSUE-Brain;
MEDLINE-22354683; PubMed-12466851;
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STRAIN-C57BL/6J; T
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83.3%;
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83.3%;
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yta; Liliopsida;
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Pred. No. 99;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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on functional annotation
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EMBL; AC092749; AAMUUUUU

Gramene; QBRU53; -.

R InterPro; IPR001128; Cytochrome_P450.

Pfam; pF00067; p450; 1.

DR PROSITE; PS00086; CYTOCHROME_P450; 1.

DR PROSITE; PS00086; CYTOCHROME_P450; 1.

Or PROSITE; PS00086; Oxidoreductase.
Query Match
Best Local Similarity
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Best Local
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahl B.B.,
In S.S., Koo H., Zismann V., Hslao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.O., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser (
"Oryza sativa chromosome 10 BAC OSJNBa0053C23 genomic sequence."
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                        PRINTS; PRO0019; LEURICHRPT.

ProDom; PD000001; Prot_Kinase; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00219; TYFKC; 1.

PROSITE; PS50502; LRR_PS; 3.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Hypothetical protein; ATP-binding; Kinase; Recep SEQUENCE 802 AA; 85525 MW; 41A650742C4C6144
                                                                                                                                                                                                                                                            STRAIN-CV. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Overton II L.L., Bera JJ., Tsitrin T., Krol M.I., Jarrahi B.B.,
Iln S.S., Koo H., Zismann V., Hslao J., Blunt S., Vanaken S.S.,
Itterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBb0038A07 genomic sequence.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC012389; AAM88626.1;
EMBL; AC012389; AAM894518.1;
Cramene; Q81404; -.
Cramene; Q81404; -.
                                                                                                                                                                       InterPro; IPR001611; LRR.
InterPro; IPR007099; LRR. plant.
InterPro; IPR00719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkin
InterPro; IPR001245; Tyr.pkinase.
Pfam; PF00069; pkinase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT 2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative receptor-like protein kinase (Hypothetical
OSJNBA0053C23.12 OR OSJNBB0038A07.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group). Eukaryota; Viridaiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopside Ehrhartoideae; Oryzaae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=39947;
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97.1%;
83.3%;
                                                                                                                                                                                                     Prot_kinase.
Ser_thr_pkinase.
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83.3%;
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Pred. No. 1.2e
1; Mismatches
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.2e+02;
                                           Receptor; T
C6144 CRC64;
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O FAMILY.
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Score Pred.

33; No.

DB 10; 1.8e+02;

Length

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Page 6
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RESULT 15
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Search completed: August 20, 2003, 12:40:38 Job time : 14.4605 secs
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                                                                                                                       Query Match 94.1
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                 "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";

Mesorhizobium loti.";

DNA Res. 7:331-338(2000).

EMBL; AP002996; BAB48475.1; ...

InterPro; IPR000843; HTH_LacI.

InterPro; IPR001761; PeriplaBP/Lac1.

Pfam; PF00532; Peripla_BP_like; 1.

SMART; SM00354; HTH_LACI; 1.

Complete proteome.

SEQUENCE 331 AA; 36699 MW; B50DDFFF8798F9A2 CRC64;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIR-MARF303099;
MEDLINE-21082930; PubMed=11214968;
MEDLINE-21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Watanabe A., Kigokawa C., Kohara M., Matsumoto M., Matsuno A.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto S., Sugimoto M.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Tabata S.;
Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q98L18
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MLR1005.
                                                            1 TGRIPP 6
|||:||
311 TGRLPP 316
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191 TGRVPP 196
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                                                                                                                       94.1%; Score 32; DB
83.3%; Pred. No. 1.2e
tive 1; Mismatches
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                                                                                                                                         DB 16; Length 331;
1.2e+02;
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Result
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                  608
608
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564.5
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                                                                                                                                                                                                                                                                                 Score
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Match
           100.0
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608
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Gapop 10.0 , Gapext 0.5
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*SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:

*SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:

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                 VH component of an Human scFV L19 ant An antibody with i Human novel protei Human novel protei Fibronectin isofor HSA antibody relat A single chain antibudy relations.
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OESS	98US-	-0M66	•			body; ED-B domain epi is; vascular prolifer d macular degeneratio ulation; blood vessel is-related pathology.	t of an	(first		standard;		88.5 .5	88.7	88.7	88.7	88.8	88.8	88. 8	88.9	88.9	89.0	89.0	89.1 89.0	89.1	89.2	89.3 89.2	89.5	89.5	89.7 80.6	89.9	90.6	91.6	91.8
ISCHE T	0075 0300	-EP03210				B domain	antibody	entry		Peptide;		221 118	281	120	120	293	240	240	240	240	367	239	217	123	121	22 <b>4</b> 121	222	120	245 220	217	240	177	116
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HOCHSCHULE ZUERICH.				٠		epitope; fibronectin; marker; iferation; diabetic retinopathy; ation; tumour; immunoscintigraphic.d ssel occlusion; ocular anglogenesis; ogy.	with improved specificity			116 AA.	ALIGNMENTS	ABR01506 AAO18441	AAW27560	ABJ18675	AAEU/UL3 AAW27553	AAG65715	AAB46039	AAB46010	AAI 15125 AAU79563	AAY15124	ABP55467	ABP45911	ABR01504	AAE07019	ABP56507	ABR01511 AAF07029	AAW13520 ABR01515	AAE07022	AAB67620	ABR01509	AAB46042	ABJ36939	ABG69320
						); marker; etinopathy; scintigraphic detection; ur anglogenesis;	city for fibronectin.					Human anti-TIMP-1 Anti-GD2 antibody	Anti-TRAIL-R antib Consensus single c	Antibody library r	Human heavy chain		Human TF anti-idio	Human MUC-1 scFv	Anti-murine CTLA-4 Monoclonal scFv an	Anti-human CTLA-4	Human TF anti-idio	Human BLyS binding	Human anti-TIMP-1	Human anti-HER2/no	Human anti-Fc-epsi	Human anti-TIMP-1	3	Human heavy chain	leukocyte	Human anti-TIMP-1 Human anti-TIMP-1	nti-1di	Antibody screening	Antibody DP47 heav

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents the VH component of a modified human scFV antibody which has specific affinity for a characteristic epitope of the ED-B domain of fibronectin. The affinity of the antibody for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10;
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                                                                                                                                                                                                                                                                        coagulant; ED-B domain; fibronectin; tumuor; ocular disorder; psoriasis; vascular proliferation; rheumatoid arthritis; blood vessel occlusion; angiogenesis; blood coagulation; variable heavy chain; VH.
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 An antibody,
ED-B domain
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                                              2001-541701/60
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   affinity for a characteristic for the treatment of diseases
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Pred.
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smatches 0;
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    epitope of the characterized
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                                                                                                                                                                                                                                                                                                                                                                                   angiogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                     scrv; antibody; ED-B domain epitope; fibronectin; marker;
angiogenesis; vascular proliferation; diabetic retinopathy;
age-related macular degeneration; tumour; immunoscintigraphic detection;
blood coagulation; blood vessel occlusion; ocular angiogenesis;
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28-APR-1999;
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                                Claim 10;
                                                                           Fibronectin
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                              Page -; 59pp; English.
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99US-0300425.
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Pred. No. 5.8e-49;
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Matches 116
                                         Isolated polypeptides useful for treating anti-inflammatory diseases nervous system disorders, and for regenerating bone and cartilage -
           Example 4;
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                                                                                                                                                     AAS22530
                                                                                                                                                                                                                                                                                        HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
                                                                                                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKDEPYEDYWGQGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
        575;
                                                                                                                                                                                                                                   Drmanac RT
894pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 608;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
.3e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an
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RESULT 5
AAU14228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to polynucleotides encoding novel human CC proteins or their active domains. The polypeptides, polynucleotides and CC antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant CC protein expression or activity. The polypeptides can be used as CC The polypeptides are used to identify compounds which bind to the CC primers, for sequencing, for chromosome or gene mapping, in the CC primers, for sequencing, for chromosome or gene mapping, in the CC primers, for sequencing, for chromosome or gene mapping, in the CC primers, for sequencing, for chromosome or gene mapping, in the CC protection of recombinant proteins, and in generating anti-sense DNA or CC target drugs to a tumour, in assays to determine biological activity, to CC protein levels, as tissue markers, and to isolate receptors or ligands. CC contraceptives of the invention may also be useful in treating plands. CC disorders, stem cell disorders, regenerating bone, cartilage, tendon, the proliferation, differentiation and survival of stem cells, as a CC contraceptive, treating osteoarthritis, anaemia, CC scherosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, altergy, asthma, CC graft-versus-host disease, eczema, haemophilia, thrombosis, and infection.

The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 116;
 Tang
                                                                                                                                                                                                                        immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                  25-JAN-2000;
                                                                                                                                                                        WO200155437-A2
                                  (HYSE-)
                                                                                                 25-JAN-2001; 2001WO-US02623
                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                           Human novel protein #99.
                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU14228 standard; Protein; 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
   YT,
                                                                                                                                                                                                                                                                                                                              novel protein; Antianaemic; osteopathic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                  HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFDYFDYMGQGTLVTVSS 116
Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 AA;
                                                                    2000US-0491404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
 Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
 RŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 608; DB 22;
Pred. No. 1.7e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307;
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Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc molecular weight markers, food supplements, and in antibody production.

CC The polypeptides are used to identify compounds which bind to the

CC polypeptides. Polynucleotides of the invention are used as probes and

CC primers, for sequencing, for chromosome or gene mapping, in the

CC production of recombinant proteins, and in generating anti-sense DNA or

CC RNA and in gene therapy. Polypeptides of the invention can be used to

CC raise antibodies/elicit an immune response, to determine duantitative

CC raise antibodies/elicit an immune response, to determine quantitative

CC raise antibodies/elicit an immune response, to determine quantitative

CC raise antibodies/elicit an immune response, to determine quantitative

CC raise antibodies/elicit an immune response, to determine quantitative

CC raise antibodies/elicit an immune response, to determine quantitative

CC raise antibodies/elicit an immune response, to determine quantitative

CC raise antibodies/elicit an immune response, to determine quantitative

CC rigament and/or nerve tissue, wound healing, treating burns, promoting

CC ilgament and/or nerve tissue, wound healing, treating burns, promoting

CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,

CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,

CC contraceptive, parkinson's and Huntington's diseases, amylotrophic lateral

CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or

CC fungal infection or from autoinmunity, cancer, allergy, asthma,

CC anti-inflammatory diseases, nervous system disorders, and infection.

CC The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as protein expression or activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 577; 894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS22533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                           ABB05053;
                                                                                                                                                                                                                                                                                                                                                                                                 ABB05053 standard;
                                                                                                                                                                                                                     angiogenesis;
                                                                                                                                                                                                                                          Fibronectin
                                                                                                                                                                                                                                                                               Fibronectin
                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                                            08-JUN-2001; 2001WO-EP06533.
                                                                                                                                          WO200196599-A2
                                                                                                                                                                                Unidentified
                        15-JUN-2000;
                                                                                                     20-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-451939/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                     isoform B; B-FN; extra domain B;
s; neoplasia; tumour; detection.
                                                                                                                                                                                                                                                                                 isoform
                                                                                                                                                                                                                                                                                                                    (first entry)
                        2000US-211677P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                 B specific binding antibody VH domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 608; DB 2
Pred. No. 2e-48;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                ED-B; antibody; VH domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method of by the aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Detecting fibronectin isoform B in body fluid of an individual, by binding fibronectin to gelatin on solid support, and determining ability of specific binding member for Extra Domain B to be retained support -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PHIL-)
(CAST/)
(ZARD/)
                                                         for quantitating the amount of an insoluble marker protein in a sample of tissue or tumour; for determining the grade or severity of neoplasia in a sample of tissue or tumour. An elevated level of B-FN in a body fluid such as plasma, cerebral-spinal fluid or cystic fluid obtained from an individual is indicative of the presence of a tumour in the individual. The methods are useful in diagnostic and prognostic individual. The methods can be readily applied to small biopsy samples situations. The methods can be readily applied to small biopsy samples obtained in the clinic, thereby providing valuable information without additional compromise to the patients or complications for the clinicians. The present sequence represents the VH domain of a B-FN ED-B specific binding antibody molecule, which is used in the exemplification
                                                                                                                                                                                                                                                                                                      The present invention describes a method for detecting the presence of fibronectin isoform B (B-FN) in body fluid of an individual. The method involves passing the fluid over a solid support (SS) to which gelatin that binds FN is attached, such that if FN is present, it is retained on SS by binding gelatin, and determining the presence of B-FN on SS by determining the ability of a specific binding member for extra domain B (ED-B) of B-FN to be retained on SS. The method is useful for the grantitative determination of B-FN in a body fluid taken or collected quantitative determination of B-FN in a body fluid taken or collected grantitative in the amendation of B-FN in a sample from an individual. Other methods from the present invention can be used:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Castellani P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZIJL/)
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-098076/13.
DB; ABA92717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHILOGEN SRL.
CASTELLANI P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZARDI L.
ZIJLSTRA A.
                                             present invention.
       117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 54; 72pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zardi
       AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ľ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zijlstra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English
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on

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RESULT 7
                              ABP95999
                     ABP95999 standard; Protein;
ABP95999;
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밁 Š В

Matches Query Match Best Local

113;

Conservative

Similarity

92.8%;

Score 564.5; Pred. No. 6.4e 0; Mismatches

0.4e-45; 0; DB 23;

> Indels Length 117;

7;

Gaps

60

116 60 μ.

01-MAY-2003 HSA antibody related VH chain VH dummy.

(first

entry)

antiinflammatory; antianaemic; immunosuppressive; neuroprotective; dual-specific ligand; cancer; HIV infection; hepatitis; rubella; anaemia; inflammation; autoimmune disorder; multiple sclerosis; Crohn's disease; Ligand; human serum albumin; myasthenia gravis. HSA; antibody; cytostatic;

Homo sapiens Synthetic.

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RESULT 8
AAYO2472
ID AAYO
XX AAYO
AC AAYO
XX IS-J
DT 15-J
XX Scre
KW Scre
KW enr1
XX W11
XX W12
XX W16
XX W099
PN W099
PD 29-A
XX
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                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a dual-specific ligand (I) comprising:

(C (a) a first single immunoglobulin variable domain with a binding

Specificity to a first antigen or epitope; and (b) a second complementary

immunoglobulin single variable domain with a binding activity to a second

C antigen or epitope. The binding domains are mutually complementary, and

c antigen or epitope. The binding domains are mutually complementary domains that

C antinflammatory, immunosuppressive and neuroprotective activities. The

C diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia,

C diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia,

C diseases or myasthenia gravis). The dual-specific ligand may be used to

C albumia (HSA) related antibody VH sequence represents a human serum

from the present invention
                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                    W09920749-A1
                                                             Unidentified
                                                                                   Screening; functional polypeptide; enrichment; single chain antibody;
                                                                                                                       A single chain antibody (ScFv).
                                                                                                                                                                                                  AAY02472 standard; Protein;
                                                                                                                                                       15-JUL-1999
                                                                                                                                                                                 AAY02472;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dual-specific ligand having immunoglobulins with binding specificity different antigens or epitopes, useful for treating, preventing or diagnosing diseases, e.g. cancer, HIV infection, inflammations, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; F1g 3; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Winter G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2001; 2001GB-0015841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-210246/20
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                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                          al Similarity 92.;
107; Conservative
                                                                                                                                                                                                                                                                                                                         1
                                                                                                                                                                                                                                                             ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFDYFDYWGOGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                               116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ignatovích O,
                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              A,
                                                                                                                                                                                                                                                                                                                                                                                     92.4%;
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                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                         <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                  Score 562; DB 24;
Pred. No. 1.1e-44;
                                                                                                                                                                                                       ₹
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                    ligand; non-functional;
ScFv.
                                                                                                                                                                                                                                                                                                                                                                         4.
                                                                                                                                                                                                                                                                                                                                                                                             Length 116;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 9
ABP95597
ID ABP9
XX ABP9
XX ABP9
XX ABP9
XX Huma
DE Huma
XX Liga
KW Anti
KW Anti
KW Guali
KW 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a method for screening for functional C polypeptides which bind a ligand. The method comprises contacting a crepertoire of polypeptides with a generic ligand, and then screening selected functional polypeptides with a target ligand. The method comprises contacting a contacting and then screening selected functional polypeptides with a target ligand. The method comprises the removal from a chosen repertoire of polypeptides, those compression of the introduction of the introduction of the compression of the compre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 92.2
28-JUN-2001; 2001GB-0015841
                                                               28-JUN-2002; 2002WO-GB03014
                                                                                                                                                 09-JAN-2003
                                                                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                             Ligand; human serum albumin; HSA; antibody; cytostatic; anti-HIV; antiinflammatory; antianaemic; immunosuppressive; neuroprotective; dual-specific ligand; cancer; HIV infection; hepatitis; rubella; anaemia; inflammation; autoimmune disorder; multiple sclerosis;
                                                                                                                                                                                                                            WO2003002609-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human serum albumin antibody related protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                      Crohn's disease; myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP95997 standard; Protein; 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2; 67pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening for functional polypeptides which bind a ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-1997;
20-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tomlinson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVOLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSYGAFDYWGQGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Winter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0066729.
97GB-0022131.
97US-0065428.
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-:
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Pred. No. 2.4e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
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The present invention describes a dual-specific ligand (I) comprising:

CC (a) a first single immunoglobulin variable domain with a binding

CC specificity to a first antigen or epitope; and (b) a second complementary

CC immunoglobulin single variable domain with a binding activity to a second

CC antigen or epitope. The binding domains are mutually complementary, and

CC the first and second domains lack mutually complementary domains that

CC share the same specificity. (I) has cytostatic, anti-HIV, antianaemic,

CC antiinflammatory, immunosuppressive and neuroprotective activities. The

CC diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia,

CC inflammations or autoimmune disorders (e.g. multiple sclerosis, Crohn's

CC diseases or myasthenia gravis). The dual-specific ligand may be used to

CC recruit cytotoxic T-cells to a cancer cell. The dual-specific ligand is

CC also useful for monitoring the efficacy of drugs, as well as for

CC also useful for monitoring the efficacy of drugs, as well as for

CC also where the present sequence represents a human serum

CC albumin (HSA) related antibody sequence, which is used in an example
RESULT 10
AAU14320
ID AAU14
XX AAU14
AC AAU14
XX 24-OC
DT 24-OC
XX Human
XX Human
KW Human
KW inmuur
KW anntid
KW anntid
KW enrki
KW enrki
KW thron
OS Homo
OS Homo
OS 9N WO200
XX U25-JJ
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dual-specific ligand having immunoglobulins with binding specificity different antigens or epitopes, useful for treating, preventing or diagnosing diseases, e.g. cancer, HIV infection, inflammations, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-210246/20.
N-PSDB; ABZ76706.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                       Human novel protein #191
                                                                                                                                                                                                                                                                                                           24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                           AAU14320 standard; Protein;
                                                                                                                                                                                                                                       Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
                                   02-AUG-2001
                                                                     WO200155437-A2
                                                                                                      Homo sapiens.
                                                                                                                                        tissue
                                                                                                                                                                                          antibacterial;
                                                                                                                                                                                                        anticonvulsant;
                                                                                                                                                        Parkinson's disease;
                                                                                                                                                                      thrombolytic;
                                                                                                                                                                                                 immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antivi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ب
                                                                                                                                        regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQLLESGGGLYOPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                        immunogen; antibody; gene ther
lisease; inflammatory disorder;
ration; immune disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                          antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.4%;
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                                                                                                                                                                      antibody; gene therapy; neurological disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                313 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 562; DB 24;
Pred. No. 2.4e-44;
5; Mismatches 4;
                                                                                                                                                                                          dermatological; haemostatic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                               osteoporosis,
                                                                                                                                                                                                                 antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116
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                                                                                                                                                                                                                                    antibodies raised against the polypephiums are used in all the contract of a mammal and prevention of disorders caused by the aberrant CC protein expression or activity. The polypeptides can be used as CC molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the CC primers, for sequencing, for chromosome or gene mapping, in the CC primers, for sequencing, for chromosome or gene mapping, in the CC production of recombinant proteins, and in generating anti-sense DNA or CC RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to CC target drugs to a tumour, in assays to determine biological activity, to CC target antibodies/elicit an immune response, to determine quantitative cC protein levels, as tissue markers, and to isolate receptors or ligands. CC protein levels, as tissue markers, and to isolate receptors or ligands. CC disorders, stem cell disorders, regenerating bone, cartilage, tendon, CC disorders, stem cell disorders, wound healing, treating burns, promoting CC ligament and/or nerve tissue, wound healing, treating burns, promoting CC alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral CC contraceptive, treating osteoporosis and osteoarthritis, anaemia, CC graft-versus-host disease, eczema, haemophilia, thrombosis, and infection. CC The present sequence represents a protein of the invention.
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                                                                                                                     Matches
                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of antibodies raised against the polypeptides are used by the aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 630-631; 894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-451939/48
                                                                                                                                                                                                      Sequence
                                                                                                                                            Local
                                                                                                                           109;
                                            61
      61
                                                                                 Н
                                                                                                                                            Similarity
                                                                                                                                                                                                        313
                                                                                                                         Conservative
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                                                                                                                                                                                                        AA;
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                                                                                                                                              92.2%;
                                                                                                                           4;
                                                                                                                           Score 560.5;
Pred. No. 4.3e
4; Mismatches
                                                                                                                                                560.5;
No. 4.3
                                                                                                                                                   3e-44;
                                                                                                                                                                        DB
                                                                                                                                                                        22;
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                                                                                                                                  Indels
                                                                                                                                                                    Length
                                                                                                                                                                          313;
                                                                                                                                    11;
                                                                                                                                    Gaps
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RESULT 11
ABG69320
ABG69320 standard; Protein; 116
                                                                                                                                   121
                                                                                                     110
                                                                           181
                                                                                                                                                 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFP------
                                                                                                                                                                                                           EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
                                                                                                                                  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSHPGYYYDSSGYSYYFDYWGQG
                                                                                                                                                                                          EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                           TLVTVSS
                                                                                                       TLVTVSS 116
                                                                            187
                                                                                                                                                                         --YFDYWGQG
                                                                                                                                                                                                     120
                                                                                                                                                                                                                                 60
                                                                                                                                                                         109
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ABG69320;

Antibody DP47 heavy chain variable region.

(first entry)

Sequence arrayed library; SAL; antibody library; protein identification;  $\mathtt{DP47}$ ;  $\mathtt{DPK22}$ .

25-JAN-2001; 2001WO-US02623

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RESULT 12
AAO21548
ID AAO21
XX AAO20
XX Unide
XX
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Best Local S
Matches 107
                                                                                                                                                                                                                                                                                                                                                       Screening antibody; 2-D electrophoresis; antibody library; proteomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in an objective structure sample containing a protein group in high efficiency, comprising reacting an objective structure sample containing a protein group or a portion containing an objective protein in the sample with an antibody library, recovering the antibody combined with the protein, replicating the recovered antibody and reacting it with the objective protein at least once. The method is used for the identification of an objective protein. The present sequence is an antibody chain (derived from the DP47 heavy chain, the DPK22 light chain) used in the method of the invention.
                                                                                                                                                  05-JUN-2001; 2001WO-JP04732
                                                                                                                                                                                                                                                                                                          Unidentified
               (NISC-) JAPAN SCI & TECHNOLOGY CORP.
(NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY
                                                                                               24-NOV-2000;
                                                                                                                                                                                                     30-MAY-2002
                                                                                                                                                                                                                                                       WO200242774-A1
                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody screening method related protein VH(DP-47).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA021548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAO21548 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening of an antibody used protein in high efficiency .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-2000; 2000JP-0373259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Sim
hes 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-579732/62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK99213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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nilarity 92.2%;
Conservative
                                                                                               2000JP-0358539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry
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Pred. No. 2.5e-44;
; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOCHO
                                                                                                                                                                                                                                                                                                                                                                          plural protein; protein spot;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 116;
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RESULT 13
ABJ36939
ID ABJ36
XX ABJ36939
AC ABJ36
XX ANT1
DE ANT1
XX ANT1
KW Human
KW Human
KW Human
KW Human
KW Human
KW Human
KW Oend
KW Human
KW Oend
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XX Univ
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                                                                                                                                                                              27-APR-2001; 2001WO-US13672.
11-MAY-2001; 2001JP-0142482.
05-OCT-2001; 2001JP-0310535.
26-OCT-2001; 2001US-0040244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for screening an antibody, comprising performing 2-D electrophoresis on plural proteins in a sample individual protein spots are separated by reacting them with an antibody library and then replicating the bound antibodies before reacting them with the spot proteins again. The method is useful for screening an antibody specific for a target protein, e.g. from a phage antibody library, which is useful in proteomics for studying various protein and complementary decayribonucleic acid (cDNA) expression libraries as well as gene functions, and in other biological and medical sciences. This sequence is a protein relating to the antibody screening method of the
  N-PSDB; ABT31881
                          WPI; 2003-120463/11
                                                                             Mikayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease;
                                                                                                                                (KIRI ) KIRIN BEER KK.
                                                                                                                                                                                                                                                                                                                                                                     07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antiallergic; haemostatic; human CD40; IL-12; LPS; lip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening an antibody using 2-D electrophoresis samples for separating individual protein spots antibody library useful in proteomics and other
                                                                                                                                                                                                                                                                                                               26-APR-2002; 2002WO-JP04292
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200288186-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-CD40 monoclonal antibody related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABJ36939 standard; Protein; 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 78pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human CD40; IL-12; LPS; lipo
dendritic cell; high G28-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoactivator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-471742/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 AA;
                                                                             Yoshida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-tumour agent;
se; coagulation fac
                                                                             Ħ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.8%;
92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ic; immunomodulator; cytostatic; a lipopolysaccharide; IFNgamma; int lipopolysaccharide; IFNgamma; s. C. CD5 expression; high G28-5; umour agent; immunosuppressant; all gulation factor VIII inhibitor; an
                                                                             Force
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 558; DB Pred. No. 2.5e 4; Mismatches
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A
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.5e-44;
                                                                             Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B cell line;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116
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Disclosure; Page 11; 36pp;

German.

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RESULT 14
AAB46042
ID AAB46
XX AAB46
XX AAB46
XX AAB46
XX MUC1
XX MUC1
XX MUC1
XX AAB4
XX MUC1
XX AAB4
XX MUC2
XX AAB4
XX AAB4
YA AAB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an antibody to human CD40, or its functional fragment, has at least one of the following properties: acting on dendritic cells to produce II-12 in the presence of LPS (lipopolysaccharide) and IrNgamma (interferon gamma); acting on dendritic cells to activate maturity of the dendritic cells with high G28-5 antibody; and activating CD95 expression with high G28-5 antibody against B cell line. Such antibodies or functional fragments can be used as immunoactivators, anti-tumour agents, immunosuppressants, and as remedies for autoimmune diseases, allergy or coagulation factor VIII inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer; antiidiotypic antibody; cytostatic; virucidal; antibacterial; TF antige antiparasitic; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-CD40 monoclonal antibody with antagonist/agonist or functional fragment, is useful in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      syndrome. This sequence represents a protein relating to the anti-CD40
                                                       Vaccines against conformation-dependent or non-peptide antigens, on DNA encoding peptide which mimics the antigen, useful e.g. as
                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB46042;
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                                                                                                                                                                                        Goletz
                                                                                                                                                                                                                                         (DELB-)
                                                                                                                                                                                                                                                                                              27-MAY-1999;
09-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                           29-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200073430-A2
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                                                                                                                                                                                                                                         DELBRUECK CENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVSS 116
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                                   vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody of the invention
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                                                                                                                                                                                                                                                                                                                                                                           2000WO-DE01809
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99DE-1043016.
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                                                                                                                                                                                                                                         MOLEKULARE MEDIZIN MAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 557; DB Pred. No. 4.9e 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .9e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TF antigen;
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Matches 105; Query Match Best Local

Similarity

90.6%;

Conservative

6;

Pred. No. 2.56 5; Mismatches Score 551; DB 22; Pred. No. 2.5e-43;

Length 240; Indels

0;

Gaps

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cor an antigen binding molecule; and (b) immunologically minics the conformation dependent, and has an immunologically minics the conformation-dependent, and has an immunologically minics the conformation-dependent, and has an immunologically minics the conformation-dependent and has an immunologically minics the conformation of amino acids. (1) is used in the form a specific spatial conformation of amino acids. (1) is used in the form a conformation of mino acids. (1) is used in the form a conformation of an analysis which are not proteins or periodes, as defined above but which have epitopes which show an accorresponding vaccine (V2) against antigens which are not proteins or peptides, as defined above but which have epitopes which show an accorresponding vaccine (2) preparing (V1) and (V2); (3) human and conformation epitope antihology fragments against the MUC1-conformation epitope antihology fragments against the MUC1-conformation epitope antihology one of 31 approximately 60 residue amino acids sequences, all fully in the specification; (4) MUC1-conformation epitope mimics and sequences of 69-17 residue amino acid sequences, all fully in the conformation one of 52 7-13 residue amino acid sequences, all fully defined in the specification; (6) TF carbobydrate epitope mimics conformation; and (7) DNA sequences and fully defined in (2) the specification; and (7) DNA sequences and (2) are used to treat concer, and infectious diseases, e.g. caused by prions, viruses, bacteria and parasites. The vaccines are effective in cases where vaccination has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encodes a region of an antiidiotypic antibody (Ab2) or another peptide which: (a) specifically binds to the binding site of an antibody (Ab1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conformation-dependent antigens (CDA) comprising antibody, or peptide which immunologically imitat
Sequence
                                                    not been
  240
  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               describes
                                                    possible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a novel vaccine (V1) against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunologically imitates CDA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (I) and/or
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RESULT 15 ABR01519 B ΩV δÃ Вþ 61  $\vdash$ 1 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGOGTLVTVSS 116 EVQLLESGGGLVQPGGSLRLSCAASGFTESSFSMSWVRQAPGKGLEWVSSISGSSGTTYY EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSITELGRSTQY 60 60

ABR01519 standard; Protein;

16-APR-2003 (first entry)

Human anti-TIMP-1 antibody heavy chain #17.

Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer;

idiopathic pulmonary

fibrosis;

WO200286085-A2

31-OCT-2002

24-APR-2002; 2002WO-US12801

24-APR-2001; 2001US-285683P

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Search completed: August 20, 2003, 12:33:39 Job time: 256.06 secs
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                                                                                                                                                                                                                                                                                          The invention relates to a novel purified preparation of a human CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1) CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of CC TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and CC invention has hepatotropic, cytostatic, nephrotropic and cardiant CC invention has hepatotropic, cytostatic, nephrotropic and cardiant CC activity. The human antibody is useful for decreasing an MMP-inhibiting CC symptoms of a disorder in which TIMP-1 is eleverating the CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic CC succest. The antibody is also useful for detecting a TIMP-1 in a test corporation, or in diagnosing a disorder in which a TIMP-1 level is clevated. The sequences shown in ABRO1502-ABRO1545 represent the heavy cxx chain regions of a human anti-TIMP-1 antibody of the invention.
                                                                                                                                                                                                   Query Match 90.3%;
Best Local Similarity 89.7%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-129114/12.
N-PSDB; ABZ74790.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FARB ) BAYER CORP. (MORP-) MORPHOSYS AG.
                                                           \vdash
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                                                                                                                           220 AA;
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Pred. No. 3.4e-43;
7; Mismatches 5;
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                                                                                                                                                                                                    5.
                                                                                                                                                                                                                                   Length 220;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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          562
552:57
542:55
541:55
540:55
539:50
539:50
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        100.0
92.4
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Match
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Gapop 10.0 , Gapext 0.5
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608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVQLLESGGGLVQPGGSLRL.....AKPFPYFDYWGQGTLVTVSS 116
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/cgn2_6/ptodata/1/pubpaa/US099_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US099_NEW_PUB_DEP:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
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                  US-09-968-561A-2
US-10-968-744A-2
US-10-040-244-16
US-10-269-805-59
US-09-840-459-85
US-09-840-459-82
US-09-880-748-1922
US-09-880-748-1922
US-09-818-247-22
US-09-818-247-26
US-09-818-247-26
US-09-840-459-76
US-10-025-687-4
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US-09-192-854-2
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                                                                                                                                                                                                                                                         Description
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                              2, Appli
2, Appli
2, Appli
16, Appl
16, Appl
59, Appl
92, Appl
Appli
Appli
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524	524.5	524.5	525	525	525	526.5		528	528		529.5	530	531	531	531	531	531	531.5	532.5	532.5	533	533	534	534	534	٠	53	37	
86.2	86.3																											88.4	
	240																		119	119	239	118	247	246	116	449	239	224	113
11	11			11	10	10	11	10	10	13	15	Ľ	10	10	10	10	11	10	15		11	15	끄	11	10	10	1	11	9
-09-880	-09-880-748-2	S-10-11E	09-917-410-4	-09-880-748-	-09-84(	-09-840-459-8	-880-748	-09-840-459-7	-09-840-459-7	-10-039-785-5	-10-118-100-54	-09-880-748-	-09-985-442-	US-09-983-580-6	-09-956-087-	w	-09-880-748-	US-09-840-459-87	-268-501-	123-3	-880-748-	-10-001-934-39	-09-880-7	-09-880-748-197	-09-840-459-80	-09-736-371B-21	-09-880-748-2	S-09-972-65	US-09-056-160B-11
1856,	Sequence 2013, Ap	9 53 3	4 A	203		84	1420	79	77.		54 Ar	1980 A	o (	Sequence 6, Appli	ω	3. Ap.	20		e (	3 Apr	e 2022	e 39. At		1975	80	P 21 Ar	20	68	1

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfre
TITLE OF INVENTION: SPECIFI
TITLE OF INVENTION: CONTAIN
TITLE OF INVENTION: ANGIOGE
FILE REFERENCE: SCH-1733P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REȘULT 1
US-09-300-425B-19
                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                            Matches 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TYLE OF INVENTION: ANGIOGENESIS FILE REFERENCE: SCH-1733P1 CURRENT APPLICATION NUMBER: US/09/300,425B CURRENT FILING DATE: 1999-04-28 PRIOR APPLICATION NUMBER: 09/075,338 PRIOR APPLICATION NUMBER: 09/075,338 PRIOR APPLICATION NUMBER: 09/075,338 PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                              Local Similarity
61 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
                                                                                          1 EVQLLESGGGLVQPGGSLRLSCAASGETFSSESMSWVRQAPGKGLEWVSSISGSSGTTYY
                                                                 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
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BIRCHLER, Manfred
                                                                                                                                                          Conservative
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                                                                                                                                                       Score 608; DB 11; Pred. No. 7.7e-47; Mismatches 0;
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61

ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116

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; ORGANISM: Homo sapiens
US-09-192-854-2
В
                               Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09192854 Patent No. US20020068276A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09968561A Patent No. US20020164642A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides
                                                                         Matches 107; Conservative
                                                                                                               Query Match
                                                                                                                                                                                                                              SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tomlinson, Ian M
APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER FILING DATE: 1997-11-21 NUMBER OF SEQ ID NOS: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 3789/72916
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 350 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: GB 9722131.1 PRIOR FILING DATE: 1997-10-20
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/511,939 PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                   TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 240
                                                                                                                                                                                                        LENGTH: 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                             Similarity
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EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.4%;
                                                                                           92.4%;
                                                                         Score 562; DB 10;
Pred. No. 1.9e-42;
5; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 240
                                                                                                                 Length 240;
                                                                             Indels
                                                                               0;
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                                                                             Gaps
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LENGTH: 240
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/10040244 Publication No. US20030059427A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
                                        SEQ ID NO 16
LENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: GB 9722131.1 PRIOR FILING DATE: 1997-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/968,744A CURRENT FILING DATE: 2003-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
                                                                                                                                                                            PILE REFERENCE: 021286/0272501
CURRENT APPLICATION NUMBER: US/10/040,244
CURRENT ELLING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/200,601
PRIOR FILING DATE: 2000-4-28
PRIOR APPLICATION NUMBER: PCT/US01/13672
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
                                                                                                                                                                                                                                                                                                                                     APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: MIKAYAMA, TOSHIFUMI
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTI
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KIRIN BEER KABUSHIKI KAISHA APPLICANT: FORCE, WALKER F.
                                                                                                                              PRIOR APPLICATION NUMBER: 09/844,684
PRIOR FILING DATE: 2001-04-27
                                                                                        SOFTWARE:
                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 09/511,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLYTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ADSVKGRFTISRDNSKNTLYLØMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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                                                                                        PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 562; DB 12;
Pred. No. 1.9e-42;
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GENERAL INFORMATION:

APPLICANT: LaROSB, Gregory J.

APPLICANT: Horvath, Christopher

APPLICANT: Horvath, Christopher

APPLICANT: Jones, S. Tarran

APPLICANT: Jones, S. Tarran

APPLICANT: O'Berien, Siobhan H.

APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: METHODS OF USE THEREFOR

TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REFERENCE: 1055.1052-012

CURRENT APPLICATION NUMBER: US/09/840,459

CURRENT FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: PCT/US01/03537
                                                                                                                                                                                                  RESULT 7
US-09-840-459-85
US-09-840-459-85
Patent No. US20020150576A1
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Publication No. US20030124129A1
GEMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1 SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.98;
Best Local Similarity 87.88;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOTETIN-2 SPECIFIC BINDING
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 12
TYPE: PRT
                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                          114 VSS 116
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                                                                                                                                                                                                                                                                                                                                                                      ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKETISFSTFSGYFDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                                          VSS 123
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87.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 552.5; DB 15; Length 123; Pred. No. 6.7e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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APPLICANT: Newman, Walter

APPLICANT: O'Brien, Slobhan H.

APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: PCT/US01/03537
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR EILING DATE: 1090-02-03
PRIOR APPLICATION NUMBER: 09/359,193
                                                                                                                                                                                                        ; ORGANISM: HOMO US-09-840-459-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-840-459-92
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PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                      SOFTWARE: F
SEQ ID NO 92
                                                                                                     Matches 105; Conserv
                                                                                                                                                       Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version SEQ ID NO 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. US20020150576A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 106;
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                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                              LENGTH: 121
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Horvath, cm.
Walter
EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
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                                                                                                  Conservative
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                                                                                                                          89.2%;
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88.3%;
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                                                                                                Score 542.5; DB
Pred. No. 5e-41;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 544; DB 10;
Pred. No. 3.7e-41;
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                                                                                                                                                                                                                                                                                                                             3.0
                                                                                                                                                 DB 10;
                                                                                                  5
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                                                                                                  Indels
                                                                                                                                                 Length 121;
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                                                                                                Gaps
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116 S 116

61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDISWGDLEGLDYWGQGTLVTVS

ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPY-----FDYWGQGTLVTVS 115

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121

US-09-840-459-82

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US-09-880-748-1922
; Sequence 1922, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: PCT/US01/03537

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 2000-02-03

PRIOR FILING DATE: 12000-02-03

PRIOR FILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1999-07-23

PRIOR FILING DATE: 1998-07-23

NUMBER OF COM-
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Best Local (
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                                                                                                                                                        FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 1855.1052-012 CURRENT APPLICATION NUMBER: US/09/840,459
                                                                                                                                                                                                                                    APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 107
                                      PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/
                                                                                               PRIOR APPLICATION NUMBER: 60/240,816 PRIOR FILING DATE: 2000-10-17
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                                                                                                                                         PRIOR FILING DATE: 2000-06-15
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APPLICATION NUMBER:
                     FILING DATE: 2001-03-21
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Newman, Walter
Jones, S. Tarran
O'Brien, Siobhan H.
O'Keefe, Theresa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKPFP-----YFDYWGQGTLV 112
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87.1%;
60/293,499
                                        60/277,379
                                                                              60/276,248
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Pred. No. 6.3e-41;
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US-09-818-247-22
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US-10-269-805-23
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1922
LENGTH: 239
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Best Local :
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                                                                                                                                                                                                        Sequence 22, Application U Patent No. US20020102657A1
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Best Local 9
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TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
                                                 APPLICANT: Mostov, Keith E.

APPLICANT: Chapin, Steven J.

APPLICANT: Richman-Elsenstat, Janice
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Secretory
TITLE OF INVENTION: No. US20020102657A1-Stalk Region of pIgR and Methods
FILE REFERENCE: 18062E-000910US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/328,604 PRIOR FILING DATE: 2001-10-11
             CURRENT APPLICATION NUMBER: US/09/818,247
CURRENT FILING DATE: 2001-03-26
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NUMBER: WO PCT/US01/09699
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85.4%;
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Pred. No. 7.7e-41;
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Pred. No. 1.4e-40;
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CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
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SOFTWARE: FBStSEQ for Windows Version 3.0
SEQ ID NO 76
LENGTH: 125
                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                 Matches.
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PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 22
LENGTH: 288
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/121,781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 1855.1052-012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LaROSA, Gregory J.
APPLICANT: Horvath, Christop
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
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PRIOR APPLICATION NUMBER: US 60/192,197
PRIOR FILING DATE: 2000-03-27
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Similarity 84.8%;
06; Conservative
                     ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKD------FPYF---DYWGQGTL 111
ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKDIEDTAMFPYYYGMDVWGQGTT 120
                                                                ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSFTVNSGYFQHWGQGTLVTVSS 142
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                                                                                                                                                       Score 539.5; DB 1
Pred. No. 9.6e-41;
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Pred. No. 2e-40;
9; Mismatches
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; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-125-687-4
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US-10-125-687-4
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US-10-025-687-4
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CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10125687
Publication No. US20030054407A1
GENERAL INFORMATION:
                                                                                                                              Matches 105;
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CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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Best Local :
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TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
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Publication No. US20020142255A1
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TYPE: PRT
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TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
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ORGANISM: Artificial Sequence
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Search completed: August 20, 2003, Job time: 126.783 secs

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Cell 24:625-637(1981).
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Mammalia; Eutheria; Rodentia;
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DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

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Wang A.-C., Wang I.Y., Fudenberg H.
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                                                                                                                                                                                                                                                                                                       HUMAN
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                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
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                                                                                                                                        Homo
MEDLINE-81013859;
                   SEQUENCE
                                                                                                                                      heavy chain V-III
mo sapiens (Human)
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MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAIN:
OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
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115 AA;
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42, Last annotation updat
  PubMed=6774332;
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12356 MW;
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78.2%;
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Best Local
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                                                                                                      Goni F., Frangione B.;

"Amino acid sequence of the Fv region of a human monocional IgM
(protein MEA) with antibody activity against 3,4-pyruvylated
galactose in Klabsiella polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
                                                                                                                                                                                                                             P01763;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
19 heavy chain V-III region WEA.
Homo sapiens (Humman).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             888
                                                              HSSP;
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                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Amino acid sequence of the variable region of a hu location of a possible JH segment,", Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM PATIENT WITH MACROGLOBULINEMIA.
-!- SIMILARITY: Contains 1 immunoglobulin-like doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding act
GO; GO:0006955; P:immune response; NA
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               ; A02046; M3HUWE.
p; P01772; 2FB4.
G0:0005576; C:extracellular; NAS.
G0:0003823; F:antigen binding activity;
G0:0006955; P:immune response; NAS.
erpro; IPR007110; Ig-like.
                                                                           AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM MALDENSTROM'S MACROGLOBULINEMIA.
SIMILARITY: Contains 1 immunoglobulin-like domain.
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122
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                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                       PubMed=6410398;
Ig_MHC.
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72.1%;
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Pred. No. 7
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Best Local S
Matches 87
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HV3F_HUMAN
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Best Local s
Matches 89
                                                                                                                         InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin v region.
DOMAIN 1 11 115
NOW_TER 115 115
SEQUENCE 115 AA; 12379 MW;
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HSSP; P01789; 1MCP.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding act
GO; GO:0006555; F:immune response; NA
                                                                                                                                                                                                                                                                    Torano A., Putnam F.W.;

"Complete amino acid sequence of the alpha 2 heavy 19A2 immunoglobulin of the A2m (2) allotype.";

Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).

-!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2N REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.

-!- SIMILARITY: Contains 1 immunoglobulin-like dome
                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
15 heavy chain V-III region BUT.
Homo sapiens (Human)
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SMARF; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Pyrre
DOMAIN 1 112
                                                                                                                                                                                                                                                                                                                                   MEDLINE=78137069; PubMed=416441; Torano A., Putnam F.W.;
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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P01767;
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                                                                                             Similarity
EVOLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
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                                                                                                                        115
12379 MW;
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; 12256 MW;
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75.0%;
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76.7%;
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Pred. No. 4.9e
l3; Mismatches
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Pred. No. 1.7e
14; Mismatches
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1
Immunoglobulin V region.
DOMAIN 1 111
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Capra J.D., Hopper J.E.;

Capra J.D., Hopper J.E.;

"Comparative studies on monotypic IgM lambda and IgG kappa from an individual patient. III. The complete amino acid sequence of the vergion of the IgM paraprotein.";

Immunochemistry 13:995-999(1976).

-1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=77117674; PubMed=65324; Capra J.D., Hopper J.E.;
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21-JUL-1986 (Rel. 01, Last Sequence up
15-SEP-2003 (Rel. 42, Last annotation
15 heavy chain V-III region BRO.
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Mammalia; Eutheria;
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                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
15 heavy chain V-III region HIL.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                   HUMAN
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                              HV3J_HUMAN
P01771;
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  Chiu Y.-Y.H.,
          MEDLINE=79124695; PubMed=420800;
Chiu Y.-Y.H., Lopez de Castro J.A.,
                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              œ
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     Lopez
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                                                                                                                                  Chordata;
Primates;
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72.7%;
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Pred. No. 1e-37;
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                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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          Poljak R.J.;
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HV3A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                           RESULT
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Best Local
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cryoimmunoglobulin IgG Hil.";
Biochemistry 18:553-560(1979).
-!- MISCELLANEOUS: THIS CHAIN WAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
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60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                      PIR; A02045; AlHUTR.
HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activ
                                                                                                              "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), II. The amino acid sequence of the H-chain, alpha-type, subgroup III; structure of the complete IgA-molecule."; Structure of the complete IgA-molecule."; Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).

--- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.

--- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region TRO.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                         HV3A_HUMAN
P01762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mmunogiobulin V regin; Pyrrolidone carboxylic acid
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                             SEQUENCE (MYELOMA PROTEIN TRO).
MEDLINE=76023781; PubMed=809331;
                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                        Hilschmann N.
                                                                                                                                                                                                   Kratzin H.,
                                                                                                                                                                                                                                                                                                                                                                           9
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G0:0005576; C:sxtracellular; NAS.
G0:0003823; F:antigen binding activity;
G0:0006955; P:immune response; NAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFP-----YFDYWGQGTLVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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13566 MW;
                                                                                                                                                                                                                                                             Chordata;
Primates;
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Pred. No. 1e-3
13; Mismatches
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PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                              Craniata; V
Catarrhini;
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                                  Matches
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Best Local
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Best Local S
Matches 80
                                                                                                             Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv;
PROSITE; PS50835; IG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       _HUMAN
HV3T_HUMAN
P01781;
                                                                                     DOMAIN
NON_TER
                                                                                             Immunoglobulin V region.
                                                                          SEQUENCE
                                                                                                                                                                                                             PIR; A02064; M3HUGL.
                                                                                                                                                                                                                                                                                         MEDLINE=75059123; PubMed=4803843; Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.; "The primary structure of a monoclonal IgM-inmunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain type), subgroup H III. Architecture of the complete IgM-molecule. Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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21-JUL-1986 (Rel. 01, Last s
15-SEP-2003 (Rel. 42, Last a
ra heavy chain V-III region
                                                                                                                                                                                                                      1- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                      Submitted (JUN-1975)
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                               InterPro;
                                                                                                                                                        InterPro;
                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                  Hilschmann N.;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                          REVISION TO 28-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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Immunoglobulin V region; Pyrr
                                            Local
                                                                                                                                               GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity; NAS.
GO:0006955; P:immune response; NAS.
SerPro; IPR003106; Ig_MHC.
                                                                                                                                                                                                                                       MISCELLANEOUS: THIS
                                                                                                                                                                                                                                  MACROGLOBULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
                                           Similarity
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
                                                                                                                                           : IPR007110;
: IPR003006;
: IPR003596;
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116
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122 /
                                  Conservative
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                                                                                                                IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
13472 MW;
                                                                       12730 MW;
                                           72.98;
                                                                                                                                           Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.0%;
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MU CHAIN WAS
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                                                                                                                                                                                                                                                                                                                                                                                                               GAL.
                              Score 443; DB 1;
Pred. No. 1.4e-37;
0; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 444; DB
Pred. No. 1.2e
L8; Mismatches
                                                                                           IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID
                                                                      2C67CA9AAAAA1282 CRC64;
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ISOLATED FROM A WALDENSTROM'S
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RESULT 11
HV3H_HH AN
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HV05_CARAU
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Best Local S
Matches 80
                                    HV05_CARAU STANDARD; PRT; 116 AA. P19181; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 heavy chain V region 5A precursor. Carassius auratus (Goldfish). Caraniata; Verte Eukaryota; Metazoa; Chordata; Craniata; Verte
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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GO; GO:0003823; F:antigen
GO; GO:0006955; P:immune r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Mammalia; Eutheria;
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21-JUL-1986 (Rel. 01, Last s
15-SEP-2003 (Rel. 42, Last s
Ig heavy chain V-III region
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=74175307; PubMed=4208843; Florent G., Lehman D., Putnam F.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Florent G., Lehman D., Putnam F.W.;
"The switch point in mu heavy chains of human IgM immunoglobulins.";
Blochemistry 13:2482-2498(1974).
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                                                                                                                                                                                                                                                                                                                                                                 115
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2; SM00406; IGv; 1.
3; SM00406; IGv; 1.
4; PS50835; IG_LIKE; 1.
5; PS50835; IG_LIKE; 1.
6; LIKE.
6; PS50835; IG_LIKE.
7; PS500: TRONE CARBOXYLIC 1.
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122 AA;
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13166 MW;
Joldfish).
Chordata; Craniata;
~ * arvqii; Teleostei;
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65.68;
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Pred. No. 1
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PYRROLIDONE CARBOXYLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74E5B6959E84100A CRC64;
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on update)
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       Vertebrata; Euteleostomi;
.Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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RESULT 13
HV31_HVMAN
ID _HV31_H
AC P0177
DT 21-TU
DT 21-TU
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DT 21-TU
DT 21-TU
DT SEP
CE Homo
OC EUKAR
OC Mammae
OX NCB1_RN [1]
RN [1]
RN [2]

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NON_TER
SEQUENCE
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P01770;
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DOMAIN
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MEDLINE-88144476; PubMed-3125551;
Wilson M.R., Middleton D., Warr G.W.;
"Immunoglobulin heavy chain variable:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
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Dreker L., Schwarz J., Reichel W., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclon
IgGl immunoglobulin (myeloma protein Nie), I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                                                                                 Ponsting1 H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain Y-III region NIE.
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                                                                                                                                                      DISULFIDE BOND.
MEDLINE=77070267; PubMed=1002129;
                                                                                                                                                                                                                                                                                                                                                MEDLINE=77070269; PubMed=826475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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IPR003006;
IPR003596;
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Ig_MHC.
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Pred. No. 1.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V REGION 5A.
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RESULT 14
HV02_CANFA
ID HV02_C
AC P01785
DT 21-JUL
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DE GACAIS
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Best Local S
Matches 84
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pfam; pF00047; 1g; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid

Immunoglobulin V region; PyrroLIKE.

PYRROLIDONE CARBOXYLIC
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                         DOMAIN
NON_TER
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                  Pfam; PF00047; 1g; 1
SMART; SM00406; IGv;
                                                                                                                                                                                                                                PIR; A90403; MHDGMO.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wasserman R.L., Capra J.D.;
"Prinary structure of the variable
immunoglobulin heavy chains.";
Biochemistry 16:3160-3168(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-112.
MEDLINE=77242268; PubMed=407924;
Wasserman R.L., Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HV02_CANFA
P01785;
                                                 Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                    "The complete amino-acid sequence of a canine mu chain."; Mol. Immunol. 16:565-570(1979).
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 113-117.
MEDLINE=80077682; PubMed=117299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (Dog).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
1g heavy chain V region MOO.
                                                                                             PROSITE;
                                                                                                                                                                                   InterPro;
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                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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119 AA;
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       AA,
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                                                                                               IG_LIKE; 1
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    12703 MW;
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70.6%;
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                                                   IG-LIKE
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       FCE07309E0A84B35 CRC64;
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Search completed: August 20, 2003, 12:34:48 Job time: 44.1352 secs
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Best Local Similarity
Matches 82; Conserv
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Best Local S
Matches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-79223895; PubMed-111245;
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-11;
InterPro; IPR003006; Ig_MH
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THAT BINDS GALACTAN.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complementarity-determining regions.";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A02077; AVMSX4.
HSSP; P01810; 2FBJ.
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[1]
                                                                          Similarity
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13246 MW; BC34FC8F31CD41B3 CRC64;
                                                                                                                                                                                                                                                               70.6%; Score 429; DB 1; 69.5%; Pred. No. 3.6e-36; tive 15; Mismatches 19
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Ig_MHC.
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Pred. No. 2.5e-36;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Match
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Gapop 10.0 , Gapext 0.5
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608
1 EVQLLESGGGLVQPGGSLRL.....AKPFPYFDYWGQGTLVTVSS 116
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1: sp_archea:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                    sp_vertebrate: *
                                                                                                                                                                                                                     Length DB
                                                     Q96BB9
Q8TC77
Q9UL91
Q9UL91
Q9UL90
Q8WUK1
Q9HCC1
Q9HCC1
Q9YL72
Q9YS09
Q8WU38
Q9YL84
Q9UL84
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                                 096bb9 homo sapien 08tc77 homo sapien 09u171 homo sapien 09u191 homo sapien 08wuki homo sapien 08wuki homo sapien 09hcc1 homo sapien 09hcc1 homo sapien 09u172 homo sapien 09u184 homo sapien 08wu38 homo sapien 09u184 homo sapien
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Q9hcc1 r
Q9u172 h
Q9y178 h
Q9y184 h
Q9wu38 h
Q9u184 h
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Q9u193 h
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	336.5	337	337.5	939	340	340.5	342.5	343	343.5	345	346.5	353.5	3,69	370	386	392.5	398.5	398.5	400	403	411	417.5	418	420	427.5	432.5	438.5	443.5	452
								56.4				58.1	60.7	60.9	63.5	64.6	65.5	65.5	65.8	66.3	67.6	68.7	68.8	69.1	70.3	71.1	72.1	72.9	74.3
	484	145	117	61:3	116	146	119	241	117	463	125	473	124	124	124	104	521	112	298	484	437	480	95	469	486	493	131	479	473
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!	099LA6	092407	Q9QXE9	Q8VCX7	Q9UL89	Q924R8	Q9UL94	Q921A6	Q9QXF0	Q99LC4	Q9UL95	Q9D8L4	Q9N0W4	09N0W6	Q9UL92	Q9UL87	Q8N4Y9	Q9UGP3	Q9QYF0	Q8VEA0	09R1A4	091XE1	09ULB6	Q8R3V9	091207	Q8NCL6	887D60	Q91WP5	Q91Z05
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# ALIGNMENTS

O96BB9 ID O96BB9 AC O96BB9 AC O96BB9 DT O1-DEC-2001 (TrEMBLITel. 19, Created) DT O1-DEC-2001 (TrEMBLITel. 19, Last sequence update) DT O1-DEC-2001 (TrEMBLITel. 19, Last sequence update) DT O1-MAR-2003 (TrEMBLITel. 23, Last annotation update) DT O1-MAR-2003 (TrEMBLITel. 23, Last annotation update) DE Hypothetical protein. OC ENtaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC ENtaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCEL_TaxID-9606; RN (1) RP SEQUENCE FROM N.A. RC TISSUB-9-cell; RA Strausberg R.; RA Strausberg P.; RA Strausberg H.; RA Strausberg P.; RA Strausberg H.;
95BB9 9FELIMINARY; PRT; 597 AA. 95BB9; 1-DEC-2001 (TIEMBLIFEL. 19, Created) 1-DEC-2001 (TIEMBLIFEL. 19, Last sequence update) 1-MAR-2003 (TIEMBLIFEL. 23, Last annotation upda
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RESULT
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Best Local S
Matches 99
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Q9UL71:
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002
01-JUN-2002
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submilted (FEB-2002) to the EMBL/GenBank/DDBJ
EMBL; BC024289; AAH24289.1; -.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 471 AA; 51791 MW;
                     Clin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                          SEQUENCE FROM N.A. MEDLINE=98277139;
                                                                                                        Wu X.,
                                                               "Myosin-reactive autoantibodies
                                                                                  Young
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      AF035043;
                                                                                     D.C.
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                                                                                                        Liu B.,
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2 (TrEMBLrel. 21,
3 (TrEMBLrel. 23,
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                                                                                                          Van
    Immunopathol.
; AAD56279.1;
                                                                                                          PubMed=9614934;
n der Merwe P.L.
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Last annotation update)
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Pred. No. 2.4e-44;
10; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                          87:184-192(1998)
                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                          L.,
                                                                   in rheumatic
                                                                                                               Kalis
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Best Local S
Matches 97
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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 1

NON_TER 1 1 1

NON_TER 121 121

SEQUENCE 121 AA; 13154 MW
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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InterPro; IPR003006; Ig_MHC
InterPro; IPR003596; Ig_v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01772; 2FB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu X., Liu B., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Myosin-reactive autoantibodies
                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                   P01772; 2FB4
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AF035023;
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                                   61
                                                                                                                   ш
                                                                                                                                                        . Similarity 97; Conserv
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                                                                                                EVQLLESGGGLYOPGGSLRLSCAASGFTESSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK--PFPYFDYWGQGTLVTVS
                                                                             IPR003596;
                                                                                                                                                                                                                                        118
118 AA;
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                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                  IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      der
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Primates;
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79.3%;
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                                                                                                                                                                                                                                                                                                                                                      Ig-like.
Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                          12843 MW;
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                                                                                                                                                                               81.2%;
82.9%;
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                                                                                                                                                          Score 494; DB Pred. No. 1.9e 8; Mismatches
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Pred. No. 4.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalis
                                                                                                                                                                                 DB 4;
1.9e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carditis
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RESULT
OPUL90
ID U190
AC 090
A
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL
Submitted (DEC-2001); If the
EMBL BC020240, AAH202401; -.

InterPro; IPR007110; Ig-11ke.
R InterPro; IPR00306; Ig_MC.
R InterPro; IPR003596; Ig_V.

INTERPROPORTY IG IG IG IG INTERPORTY IG IG IT INTERPORTY IG IG IT INTERPORTY IG IG INTERPORTY INTERPORTY INTERPORTY IG INTERPORTY INTER
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Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pı
NCBI_TaxID=9606;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8WUK1;
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-Tonsil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8WUK1
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HSSP; P01772; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UL90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UL90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR007110; Ig-11ke.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 491.5;
Pred. No. 3.2e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>ن</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; | Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ED57FDD19086D07F CRC64;
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3.2e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
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RESULT
Q9UL72
ID Q0
AC Q0
AC Q0
DT 0
DT 0
DT 0
OC 0
OC 1
OC 1
OC 1
RP
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Best Local S
Matches 89
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Best Local S
Matches 95
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Q9HCC1;
O1-MAR-2001 (TrEMBLrel. 16, C
O1-MAR-2001 (TrEMBLrel. 23, I
O1-MAR-2003 (TrEMBLrel. 23, I
Single chain Fy (Fragment).
                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Myosin-reactive immunoglobulin heavy chain v
                                                                                                                                                                                                                                     Q9UL72
Q9UL72;
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KIKUChi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

"An antibody fragment2A3 specific for native lysozyme :Isolaion human synthetic phage display library and characterization.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB049915; BAB16829.1; --

HSSP; P01772; 2FB4.
                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                              Homo
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                       NCBI_TaxID-9606
      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                  (Fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110;
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                                                                                                                                                                                                                                                                                                     œ
                                                                                                         sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLV
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89; Conserv
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95; Conser
    FROM
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112
112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             613
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12243 MW;
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79.5%;
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79.2%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 475; DB 4;
Pred. No. 1.6e-41;
1; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 484;
Pred. No. 1
                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24F1A45EC3B84788 CRC64;
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i; Hominidae;
                                                                                                                                               s update)
lon update)
in variable
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                                                                                                        NON_TER
SEQUENCE
                                                                                                                                  InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=96071149; PubMed=7475288;

MEDLINE=96071149; PubMed=7475288;

Cao J., Vescio R.A., Rettig M.B., Hon
Lichtenstein A.K., Berenson J.R.;

TA CD10-positive subset of malignant

"A CD10-positive subset of malignant
                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Myosin-reactive autoantibodies fetus.";
                                                                                                                                                                                 myeloma using PCR with patient-specific Leukemia 9:1948-1953(1995).
EMBL; S80860; AAD11339.1; -.
HSSP; P01772; 2FB4.
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                                                                                                                         PROSITE; PS50835; IG_LIKE; 1.
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                           ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK----PFPYYFDYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPEPYF---
                                                                                                                                                                                                                                                                                                                                                                                                                             ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAFYYCARDRFGEF-LFDYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNYMNWVRQAPGKGLESV-SVTYSGGSSYY
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118 AA;
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                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                        AA;
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81.7%;
                                                                                                         15768 MW;
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73.8%;
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Last sequence up
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Pred. No. 2.8e-41;
                                                                Score 472; DB 4;
Pred. No. 4.6e-41;
7; Mismatches 16;
                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                         8489FCAAA7BC925C CRC64;
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Best Local
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ da

EMBL; BC021276; AAH21276.1; -.

Interpro; IPR007110; Ig-1ike.

Interpro; IPR003006; Ig_MHC.

Interpro; IPR003596; Ig_V.

Pfam; PF00047; Ig; 4.

SMART; SM00406; IGV; 1.

PROSITE; PS00835; IG_LLKE; 2.

PROSITE; PS00290; IG_MHC; 2.
                                                                  SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Tiu B., Van der Merwe P.L.
                                                                                                                                                                                                                                                                                                                                                                                           Q9UL84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLre Hypothetical protein.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                Myosin-reactive
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01-MAY-2000
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                               "Myosin-reactive
fetus.";
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CEMBLrel. 23, Last annot
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        87:184-192(1998)
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Catarrhini;
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SEQUENCE
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MEDLINE-98277139; PubMed-9614934;
rin B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                              PROSITE;
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SMART; SM00406; IGV;
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF035030; AAD56266.1; HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; InterPro; IPR003006;
               61
                                                 62
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                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
                                                                      DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYCAGGGGLGLGYWGQGTLVTVSS
                     DSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPY-FDYWGQGTLVTVSS 116
                                                                                                                                                                                                                                                                                          PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                     116
116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
122 AA;
                                                                                                                                                         Conservative
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12434 MW;
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\: 13579 MW;
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80.2%;
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75.4%;
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. 13, Last sequence 23, Last annotations.
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                                                                                                                                                     Pred. No. 1.366; Mismatches
                                                                                                                                                                        Score 466.5;
Pred. No. 1.
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Pred. No. 9.
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                                                                                                                                                                          .3e-40;
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.5e-41;
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RESULT 13
Q96K6
AC Q96K6
AC Q96K6
DT Q1-DE
DT Q1-MF
DE Hypot
OS HOMOO
OC Euka
OC MAMMM
OX NCBI
RN [1]
RP TIS:
RA IS:
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Best Local S
Matches 92
                                                                                                                                                                                  Pterin (Fragment).
(Fragment).
Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cr
Eukaryota; Metazoa; Rodentia; S
                                                                                                                                                                                                                                                                                                                                                                         0920E7;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
Pterin-mimicking anti-idi
                                       SEQUENCE FROM N.A.
Atkin J.D., Tape A., Jenning
"Definition of the Idiotope
in Mammalian Cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Mammary gland;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Vanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
"NEDO human CDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO27379; BAB55072.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q920E7
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003906; Ig_V.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGV; 1.
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Q96K68;
01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protean FLJ14473.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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92; Conserv
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SS 141
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494 AA; 5
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MBLrel. 19, Last sequence update)
MBLrel. 23, Last annotation update)
anti-idiotope heavy chain variable
          ç
                                                                Jennings I.G., Horaitis O.,
diotope of Pterin-Mimicking
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75.48;
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EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                 Craniata; Vertebrata;
Sciurognathi; Muridae;
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; Murinae; Mus
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Best Local S
Matches 90
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Best Local Similarity 73.9
Matches 88; Conservative
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Pfam: PF00047; 19; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

NON_TER 119 119

SEQUENCE 119 AA; 13025 MW;
                                                                                                                                                                      InterPro; IPRO03597; Ig_C1.
InterPro; IPRO0306; Ig_MHC.
InterPro; IPRO03096; Ig_V.
Pfam; PFO0047; Ig; 4.
SMART; SM00409; IG; 4.
SMART; SM00407; IGc; 2.
SMARR; SM00406; IGv; 1.
SMARR; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 499 AA; 53376 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF307937; AAL09421.1; InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                           Q8NSK4;
01-CCT-2002 (TrEMBLrel. 22, Created)
01-CCT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8N5K4
                                                                                                                                                                                                                                                                                   InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032249; AAH32249.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                   ISSUE-Blood;
                                                                                                                                                                                                                                                                                                          nterPro;
                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
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                       109
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Similarity
                                                                                                                                                                                                                                                                                                          IPR003599;
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                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13025 MW; F6E904044381CA7C CRC64;
                                                                                                                                                                           53376 MW; 93A5C89582054F32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.4%; Score 458.5; DB 11; Length 119; 73.9%; Pred. No. 8.8e-40; tive 13; Mismatches 15; Indels 3;
                                                                                                                                75.1%; Score 456.5; DB 4; Length 499; 70.3%; Pred. No. 8.9e-39; tive 11; Mismatches 14; Indels 13
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Last annotation update)
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Search completed: August 20, 2003, 12:40:11 Job time : 221.533 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                      Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                    Score
            73
73
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          100.0
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Match
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Gapop 10.0 , Gapext 0.5
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73
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// Cgn2_6/ptodata/1/paa/US086_COMB.pep: *
// Cgn2_6/ptodata/1/paa/US088_COMB.pep: *
// Cgn2_6/ptodata/1/paa/US089_COMB.pep: *
// Cgn2_6/ptodata/1/paa/US099_COMB.pep: *
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/cgn2_6/ptodata/1/paa/US997A_COMB.pep:*
/cgn2_6/ptodata/1/paa/US997A_COMB.pep:*
/cgn2_6/ptodata/1/paa/US998_COMB.pep:*
/cgn2_6/ptodata/1/paa/US998_COMB.pep:*
/cgn2_6/ptodata/1/paa/US999A_COMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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          14
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US-09-300-425B-20
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Sequence 20, Sequence 20,
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Sequence 9, Appli Sequence 800, App Sequence 93, Appl	50, Appl	equence 50, Appl	`:	equence II/435,	uence 50938,	equence 64189,	e 64613,	equence /2/, Ap	equence 727,	178822,	equence 7,	382, Ap	649,	64869,	quence 4, Ap	е :	equence 142655.	ednence 20,	equence 18, Ap	18,	equence 22, App	equence 22, App	Sequence 1, Appli	78827,	78383,	78382	78381	78365,	78364,	78362,	78361	78345,	e 20. An

## ALIGNMENTS

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RESULT 1

US-09-075-338C-20

Sequence 20, Application US/09075338C

GENERAL INFORMATION:

APPLICANT: NERI, Dario

APPLICANT: VITI, Francesca

APPLICANT: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY

FILE REFERENCE: SCH-1733

CURRENT FILING DATE: 1998-05-11

SOFTWARE: PATON NUMBER: US/09/075,338C

CURRENT FILING DATE: 1998-05-11

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATONS: 34

SOFTWARE: PATONS: Attificial Sequence

FEATURE: NFORMATION: Description of Artificial Sequence: antibody linker

US-09-075-338C-20
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Query Match
Best Local Similarity
Matches 14; Conserv

100.0%; Score 73; DB 14; Length 14; ilarity 100.0%; Pred. No. 0.04; Conservative 0; Mismatches 0; Indels

0

Gaps

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GDGSSGGSGGASTG 14

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; OTHER INFORMATION: Description of Artificial Sequence: antibody linker \mathtt{US}\text{-}09\text{-}300\text{-}425\text{B}\text{-}20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BIRCHLER, MANIFED TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin V
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 1998 (
NUMBER OF SEQ ID NOS: 34
                                    Query Match
Matches
                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: SCH-1733P2
CURRENT APPLICATION NUMBER: US/09/512,082
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 09/300,425
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGIOGENESIS FILE REFERENCE: SCH-1733P2
                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                      FEATURE:
                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: antibody linker
                                                                                                                                                                                ENGTH: 14
                   Local Similarity
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VITI, Francesca
                                                                                                                                                                                                                        PatentIn Ver. 2.1
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100.0%; Score 73; DB 1.
100.0%; Pred. No. 0.04;
tive 0; Mismatches
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Pred. No. 0.04;
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      Gaps
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 78361
LENGTH: 238
TYPE: PRT
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US-09-791-537-78345
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                                                                                                                                 RESULT 6
US-09-791-537-78362
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 78345
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                                                                                              Sequence 78362, Application US/09791537 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
             APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek
FILE REFERENCE: 261/210
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Local Similarity 100.0%;
hes 14; Conservative 0
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Pred. No. 0.
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                                                                                                                NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 78365
LENGTH: 238
TYPE: PRT
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                                 Matches
                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                 Sequence 78365, Appl GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 78364
LENGTH: 238
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/791,537 CURRENT FILING DATE: 2001-02-22
                                                                                                                                                                                                               APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
FITLE OF INVENTION: METHODS OF USE THEREOF
FILB REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 78362
LENGTH: 238
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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Llarity 100.0%; Pred. No. 0,
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US-09-791-537-78382
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US-09-791-537-78381
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; ORGANISM: Homo sapiens US-09-791-537-78381
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 78381
LENGTH: 238
TYPE: PRT
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Best Local Similarity 100.0%;
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 78380
LENGTH: 238
CURRENT APPLICATION NUMBER: US/09/791,537
                       APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                            APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
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US-09-791-537-78383
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Best Local Similarity 100.
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APPLICANT: Danzer, Joseph
APPLICANT: IDANZER, JOSEPH
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09-791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIAL OF SEQ ID NOS: 153055
SOFTWARE: DATE: 138
LENGTH: 238
TYPE: PRT
                                                                                                                                                 APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: METHODS OF USE THEREOF
TITLE OF INVENTION: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 78827
LENGTH: 238
TYPE: PRT
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TYPE: PRT
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; TYPE: PRT
; ORGANISM: HC
US-09-075-338-1
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US-09-075-338-1
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US-10-276-781-1626
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Search completed: August 20, 2003, 13:13:38 Job time : 144.289 secs
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SEQ ID NO 1
LENGTH: 299
TYPE: PRT
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GENERAL INFORMATION:
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SOFTWARE: FastSEQ for
SEQ ID NO 1626
LENGTH: 384
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CURRENT FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 1
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APPLICANT: tarli
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APPLICANT: Tang et al.
ITILE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-018 (785 contig)
CURRENT APPLICATION NUMBER: US/10/276,781
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
                                                                                                                             Local Similarity 100
es 14; Conservative
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re greater than or equal to the score of the result being printed,
18 derived by analysis of the total score distribution.
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73
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283308 seqs, 96168682 residues
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GenCore version (c) 1993 - 2003
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hypothetical glyci	hypothetical glyci	homeotic protein s	homeotic protein s	merozoite surface	merozoite surface	keratin, type I, c	hypothetical glyci	hypothetical glyci	σ		wingless receptor	homeotic protein o	hypothetical glyci	loricrin - mouse	F5D14.12 protein -

### ALIGNMENTS

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70824 В A;Gene: Rv0747 C;Superfamily: elastin A; Molecule type: DNA A; Residues: 1-801 <COL> A; Cross-references: GB:/ hypothetical glycine-rich protein Rv0747 - Mycobacterium tuberculosis (strain H37RV) C:Species: Mycobacterium tuberculosis C:Date: 17-Ju1-1998 #sequence\_revision 17-Ju1-1998 #text\_change 20-Jun-2000 Š A; Status: preliminary; nucleic acid sequence not shown; translation not shown C; Genetics: A; Experimental source: strain C; Accession: F70824 Query match
Best Local s
Matches 10 313 GNGGNGGNGGASTG 10; 1 GDGSSGGSGGASTG Similarity Conservative GB:AL021958; GB:AL123456; NID:g3261536; PIDN:CAA17514.1; PID:g291 ce: strain H37Rv 79.5%; 326 14 Score 58; Pred. No. Mismatches 4.9; 2; ۲. Length 801; Indels 0

Holroyd,

geno

Gordon

RESULT 2 F70971

0

Holroyd,

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70971
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

geno

A; Molecule type: DNA A; Residues: 1-588 <COL>

A;Cross-references: GB:AL009198; GB:AL123456; NID:g3242262; PIDN:CAA15752.1; PID:e120 A;Experimental source: strain H37Rv C;Genetics:

neat-shock

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A; Note:
A; Note:
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C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17406
R;Iranfar, N; Loomis, W.F.
submitted to the EMBL Data Library, July 1998
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C; Superfamily:
       RESULT
A70869
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Bar A;Title: Deciphering the biology of Mycobacterium tuberculosis from A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70806
                                                                                                                                                                                                                                                                             A;Experimental source: strain H37Rv
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical glycine-rich protein Rv3507 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Decies: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: E70806
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A; Residues: 1-1022 <IRA>
A; Cross-references: EMBL
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A; Accession: T17406
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C; Superfamily:
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A; Residues: 1-1381 <COL>
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83.3%;
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78.6%;
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Pred. No. 8.7;
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RESULT 7 H70663

hypothetical

glycine-rich protein Rv1840c -

Mycobacterium

tuberculosis

(strain

H37RV)

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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squar Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell A;Title: Deciphering the biology of Mycobacterium tuberculosis from the A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70869
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Shvets, Y.P.; Chumakov, I.M.; Kisselev, L.L. Mol. Biol. 24, 663-677, 1990
A;Title: Sequencing the fragment from a transcriptionally A;Reference number: PN0109
A;Accession: PN0109
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A; Residues: 1-1660 <COL>
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F;93-100/Region: 8-residue repeat
F;105-112/Region: 8-residue repeat
F;118-125/Region: 8-residue repeat
F;152-163/Region: 12-residue repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-183 <SH
C; Genetics:
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30
C;Accession: PN0109
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PN0109
В
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F;164-175/Region:
F;164-171/Region:
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F;77-84/Region: 8-residue repeat
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                                     GDGSSGGSGGASTG 14
 GGGSSGGGGGGSSG 136
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8-residue repeat
8-residue repeat
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8-residue repeat
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Pred. No.
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Pred. No. 3.9;
1; Mismatches
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23;
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3.9;
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                                                                                                                     183;
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Holroyd,
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RESULT 8
A70812
hypothetical glycine-rich protein Rv0833 - Mycobacterium tuberculosis (strain H37RV)
C.Species: Mycobacterium tuberculosis
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 07-Mar-2003
C.C.Cate 17-Jul-1998 #sequence 07-Mar-2003
C.C.Cate 17-Jul-1998 #sequence 07-Mar-2003
R.C.Cate 17-Jul-1998 #sequence not shown 17-Jul-1998 #text_change 07-Mar-2003
R.C.Cate 17-Jul-1998 #sequence not shown; translation not shown
A.C.Cate 18-ALO22004; GB:AL123456; NID:93261550; PIDN:CAA17639.1; PID:92916
A.C.Cate 18-
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C;Date: 17-Jul-12...
C;Accession: H70663
R;Cole, S.T.; Brosch
; Connor, R.; Davie;
; Connor, R.; Davie;
; Transam, M.; R
                                                                                    hypothetical glycine-rich protein Rv0746 - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis G;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 07-Mar-2003 C;Accession: E70824 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                       A;Authors: Sqares, R.; Sulston, J.E.;
A;Title: Deciphering the biology of M
                                                    Nature 393, 537-544
A; Authors: Sqares,
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987; PMID:9634230
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C;Superfamily: uncharacterized glycine-rich
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Best Local S
Matches S
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A; Residues: 1-515 <COL>
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                                           M.A.,
537-544, 15
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9; Conserv
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44, 1998
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Pred. No. 15;
3; Mismatches
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Pred. No. 10;
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                                              Taylor, K.;
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                 tuberculosis
                                              Whitehead,
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                                           B.G
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                                                                                                                                                                                                                                                                                                    C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999 (;Accession: S77300 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Io, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamadi DNA Res. 3, 109-136, 1996 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium;
                                                                                                                                                                                        A; Status: nucleic acid sequence
                                                                                                                                                                                                                        A; Reference number: A; Accession: S77300
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S77300
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Query Match
Best Local Similarity
                                                                                                               Cross-references:
                                                                                                                                   Molecule type: DNA
Residues: 1-3016 <KAN>
                                                                   Treferences: EMBL:D90907; GB:AB001339; NID:g1652618; PIDN:BAA17634.1; the nucleotide sequence was submitted to the EMBL Data Library, June
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S74322;

MUID:97061201;

PMID:8905231

not

shown;

translation

not shown

of the genome of the unicellular cyanobacterium

Yamada,

; Miyajima, W.; Yas Synechocys

74.08; 71.48;

Score Pred.

No.

DB 54;

2

Length 3016

PID:d101 1996

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hypothetical protein slr1403 - C: Species: Synechocystis sp. A: Variety: PCC 6803
                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1325 <HIM>
A;Cross-references: EMBL:AE000038; GB:U00089;
A;Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                       A;Genetic code: SGC3
C;Superfamily: Mycop
                                                                                                                                                                                                                                                                                                                                                                 R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; I Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the A;Reference number: $73327; MUID:97105885; PMID:8948633
A;Accession: $73723
                                                                                                                                                                                                                                                                                                                                                                                                                                        probable lipoprotein H08_orf1325 - Mycoplasma pneum K;Alternate names: MG309 homolog H08_orf1325 C:Species: Mycoplasma pneumoniae A;Variety: ATCC 29342 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 C;Accession: $73723
                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Accession: E70824
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Resiques: 1-783 <COL>
A;Cross-references: GB:AL021958; GB:AL123456; NID:g3261536; PIDN:CAA17513.1;
A;Experimental source: strain H37Rv
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C; Superfamily:
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RESULT 12
A47318
RNA-binding
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C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A47318
R;Michaud, E.J.; Bultman, S.J.; Stubbs, L.J.; Woychik, R.P.
Genes Dev. 7, 1203-1213, 1993
A;Title: The embryonic lethality of homozygous lethal yellow micharacteric number: A47318; MUID:93307655; PMID:8319910
A;Accession: A47318
                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
A; Gene: Merc
C; Superfamily: u
F; 22-82/Domain:
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A;Note: sequence extracted from NCBI backbone (NCBIN:134703, NCBIP:134704)
C;Superfamily: unassigned ribonucleoprotein repeat containing proteins; ri
F;22-02/Domain: ribonucleoprotein repeat homology <RRM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Duhl, D.M.; Stevens, M.E.; Vrieling, H.; Saxon, P.J.; Miller, M.W.; Epstein, Development 120, 1695-1708, 1994
A;Title: Pleiotropic effects of the mouse lethal yellow (Ay) mutation explained A;Reference number: 153142; MUID:94326666; PMID:8050375
A;Accession: I53142
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene Merc protein - mouse
C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I53142 William W. Epste
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coat protein A precursor - phage fd

(;Species: phage fd

C;Date: 30-Sep-1980 #sequence_revision 18-Aug-1

C;Accession: A04266; B04266

C;Accession: A04266; B04266

R;Beck, E.; Sommer, R.; Auerswald, E.A.; Kurz,

Nucleic Acids Res. 5, 4495-4503, 1978

A;Title: Nucleotide sequence of bacteriophage 1
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-296 <RES>
A; Cross-references: GB:S72641; NID:g619301; PIDN:AAC60688.1;
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Search completed: August 20, Job time: 11.7831 secs

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A;Cross-references: GB:V00602; GB:J02451; GB:A;Experimental source: strain 478, Heidelberg R;Goldsmith, M.E.; Konigsberg, W.H. Blochemistry 16, 2686-2694, 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Comment: Coat protein A is necessary for adsorption of the end of the phage particle.
C;Comment: Bacteriophages fd, M13, and fl are male-specific fc;Genetics:
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A; Accession: A04266
A; Molecule type: DNJ
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F; 19-424/Product:
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C;Comment: Bacteriophages fd, Ml3, and fl
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                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: phage M13
C;Date: 31-Dec-1991 #sequence_revision 31-Dec
C;Accession: C04266; A04266
C;Accession: C04266; A04266
R;van Wezenbeek, P.M.G.F.; Hulsebos, T.J.M.;
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A; Residues: 1-24, 'P', 26,
                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-424 < VAN>
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                                    1 GDGSSGGSGGASTG
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llarity 71.4%;
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                        seq length: 0 seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen
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YD25_MYCTU
HMCC_DROME
FRZ2_DROME
Z281_HUMAN
SHK1_HUMAN
SHK1_HUMAN
SHX1_MOUSE
ST23_HUMAN
COAT_PAVC2
UN37_CAEEL
K2C1_MOUSE
COAT_PAVC7
COAT_PAVC7
COAT_PAVC9
COAT_PAVCB

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Y140_MYCTU
Y309_MYCDN
RALY_MOUSE
COAA_BPFD
COAA_BPFM13
Y118_MYCTU
Y208_MYCTU
MSA2_PLAFE
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70 drosophila
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72 homo sapien
686 homo sapien
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                 RESULT 1
Y747_MYCTU
ID Y747_MYCTU STANDARD; PRT; 801 AA.
C 0538L0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-CCT-2001 (Rel. 40, Last annotation update)
DT 16-CCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical PE-PGRS family protein Rv0747 precursor.
GN RV0747 OR MT0772.5 OR MTW041.21.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
EMBL; AL021958; CAA17514.1; --
EMBL; AE006508; AAK45011.1; --
PIR; F70824; F70824; F70824
TIGR; MT0772.5; --
TubercuList; Rv0747; --
InterPro; IPR000084; PE_region.
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P23490 homo sapien P17275 homo sapien O89114 mus musculu O95409 homo sapien P13645 homo sapien P3527 homo sapien P34689 caenorhabdi P56877 mycobacteri P48377 mus musculu P00522 drosophila Q06852 clostridium	O35740 mus musculu

## ALIGNMENTS

R OX	NCBI_TaxID=1773;
RΡ	SEQUENCE FROM N.A.
80	37Rv;
RX	MEDLINE=98295987; PubMed=9634230;
RΑ	1
RΑ	Gordon S.V., Eiglmeier K., Gas S., Barry C. TIT Tokes F.
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor B
R.	2
RA	Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy I.
R	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.
RA	Rutter S., Seeger K., Skelton S., Squares S., Squares S.,
RA	Sulston J.E., Taylor K., Whitehead S., Barrell B.G.
RT	"Deciphering the biology of Mycobacterium tuberculosis from the
RT	7
R P	Nature 393:537-544(1998).
RP P	SECUENCE FROM N A
20	STRAIN-CDC 1551 / Oshkosh:
RA	., Eisen J.A., Carpenter I. white
RA	Peterson J., DeBoy R., Dodson R., Gwinn M.L. Haft D. Halle D.,
RA	Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D. Salabera S.
RA	Delcher A., Utterback T., Weidman J., Khouri H., Gill J. Mikula a
R	Bishai W.;
RT	clinical
RT	laboratory strains.";
RL	Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
3 6	-1- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
3 6	SUBFACTOR.
88	This SWISS-PROT entry is converiable. The in section is the section of the sectio
ဂ	between the Swiss Institute of Bioinformatics and Bioinformatics and the swiss institute of Bioinformatics and the
င္ပ	the European Bioinformatics Institute. There are no restrictions on its
င်	use by non-profit institutions as long as its content is in the
S	modified and this statement is not removed. Usage by and for common way
88	entities requires a license agreement (See http://www.isb-sib.ch/announce
3 6	or send an email to license@isb-sib.ch).

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RX MEDLINE-98295987; PubMed-9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I.
RA Gordon S.V., Eiglmeier K., Gas S., Barrier T., Connor R.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Theciphering the biology of Mycobacterium tuberculosis from the
Tromplete genome sequence.";
L. Nature 393:537-544(1998).
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PE-PGRS family protein Rv1840c.
RV1840C OR MT1888 OR MTCYLAI1.04 OR MTCY359.33.
                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter Fleischmann R.D., Alland D., Eisen J.A., Carpenter Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva Delcher A., Utterback T., Weidman J., Khouri H., G
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Q50594;
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NCBI_TaxID=1773;
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                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potentianies SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                                                                     "Whole genome comparison of Mycobacterium
                        the European
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RESULT 3
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EMBL; AE007047; AAK46159.1;
PIR; H70663; H70663.
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InterPro; IPR000084; PE_region.
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                                                                                                                                                                the European Bioinformatics Institute. The European Bioinformatics Institutions as long use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-AFCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plage
                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma pneumoniae.
Bacteria; Firmicutes;
                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                     pneumoniae.";
Nucleic Acids Res. 24:4420
-:- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2104;
                                                                     CHAIN
                                                                                                                                                                                                                                                              -1- SIMILARITY: BELONGS TO THE MG307 / MG309 / MG338 FAMILY.
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                                              SEQUENCE
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(Rel. 40, Last annotation update)
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nilarity 71.4%;
Conservative
                                                                                                         protein; Lipoprotein;
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185
219
43916 N
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1325
                                                                                                                        PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                        analysis of the
                                                                                                                                                                                                                                                                                                   24:4420-4449(1996).
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                                               HYPOTHETICAL LIPOPROTEIN MG309
N-ACYL DIGLYCERIDE (POTENTIAL)
MW; 13FEF53D155ECB15 CRC64;
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                                                                                                                                                                                  is not removed. agreement (See
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  Score 54; DB Pred. No. 19; 0; Mismatches
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrinl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrinl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RT "Functional annotation of a full-length mouse cDNA collection.",
RL Nature 409:687-680707011
TISSUE-Mammary grand;

MEDLINE-22388257; pubMed-12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *Pleiotropic effects of the mouse lethal yellow explained by deletion of a maternally expressed simultaneous production of agouti fusion RNAs.", Development 120:1695-1708(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-C57BL/6J; TISSUE-Embryonic |
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-94326666; PubMed-8050375;
Duhl D.M., Stevens M.E., Vrieling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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"The embryonic lethality of homozygous lethal yellow mice (Ay/Ay)
associated with the disruption of a novel RNA-binding protein.";
Genes Dev. 7:1203-1213(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RALY_MOUSE STANDARD; PRT; 312 AA.

Q64012; Q99K76; Q9CXB6; Q9CXX6;
28-FEB-2003 (Rel. 41, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
RNA-binding protein Raly (hnrNP associated with lethal yellow
(Maternally expressed hnrNP C-related protein).
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Mammalia; Eutheria;
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; Rodentia;
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Sciurognathi; Muridae,
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gene
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Murinae; Mus
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Matches 10
                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -I- TISSUE SPECIFICITY: Widely expressed in brain, testis, lung, spleen and kidney. Weakly expressed in liver.
-I- DEVELOPMENTAL STAGE: Expressed in the unfertilized egg, in the blastocyst, as well as in the developing embryo and fetus.
-Expressed in developing skin.
-I- DISEASE: Defects in RALY are the cause of lethal yellow mutation (A(y)), a dominant allele that cause embryonic lethality when homozygous, and pleiotropic effects when heterozygous, including yellow pelage, obesity, non-insulin dependent diabetes and increased tumor susceptibility. A(y) is due to a 170 kb deletion that removes all but the promoter and non-coding first exon of RALY and links them to the ASIP/Agoutl gene.
-I- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                             PROSITE; PS00030; RRM_RNP_1; 1.
Ribonucleoprotein; RNA-binding; Nuclear protein; Alternative
                                                                                                                                                                   PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1;
                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                             EMBL; AF148458; MGD; MGI:97850;
                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                              InterPro; IPR000504; RNA_rec_mot Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sancy Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE-99431566; PubMed-10500250;
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                                                                                                                                                                                                                                                                    L; S72641; AAC60688.1; ...
L; L17076; -; NOT_ANNOTATED_C
L; AKO14356; BAB29294.1; ...
L; BC004851; AAH04851.1; ...
L; BC016587; AAH16587.1; ...
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      . Similarity
10; Conser
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281
      Conservative
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281
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125
                   72.68;
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Young A.C., Shevchenko Y., Bouffard G.G.,
man J.W., Green E.D., Dickson M.C.,
                                                               MW;
                                                                          RNA-BINDING (RRM).

Missing (in isoform 1).

/FTId=VSP_005805.

G -> S (IN REF. 2 AND 3)

T -> I (IN REF. 1).
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 Pred. No. 6.1; Mismatches
                              Score
                                                            BF68E0E8876BFC50 CRC64;
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                 DB 1;
6.1;
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STRAIN-478 / Heidelbery;
MEDLINE-79136480; PubMed-745987;
MEDLINE-79136480; PubMed-745987;
Beck E., Sommer R., Auerswald E.
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21-JUL-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE-77242231; PubMed-329863; Goldsmith M.E., Koniqsberg W.H.; Rosidsberg W.H.; Madsorption protein of the bacteriophage fd: properties, and location in the virus."; Biochemistry 16:2686-2694(1977).
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Viruses; ssDNA viruses; Inoviridae;
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Holliger P., Riec
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"Nucleotide sequence of bacteriophage 
Nucleic Acids Res. 5:4495-4503(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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SIGNAL 1
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1FGP; 16-JUN-97.
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Structure 7:711-722(1999).
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van Wezenbeek P.M.G.F., Hulsebos T.J.M.,
"Nucleotide sequence of the filamentous
comparison with phage fd.";
Gene 11:129-148(1980).
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Bacteriophage f1.
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                                                                                                                                                       Lubkowski J., Hennecke F., Plucckthun A
"The structural basis of phage display
structure of the N-terminal domains of
Nat. Struct. Biol. 5:140-147(1998).
                                                                                                                                                                                                                           SPECIES-Phage M13;
MEDLINE-98120978; PubMed-9461080;
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"Nucleotide sequence of bacteriophage
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EMBL; V00606; CAA23872.1; --
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PIR; CO4266; Z3BPM3
PDB; 1G3P; 28-JAN-98
PDB; 1G3P; 28-JAN-99
Pfam; PF05357; Phage_Coat_A; 2
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SUBUNIT: THERE ARE ABOUT FIVE COPIES OF THIS PROTEIN PER MATURE PHAGE.
DOMAIN: Consists of three domains (N1, N2, and CT). The N2 domains (N1, N2, and CT).
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MISCELLANEOUS: THEY ARE LOCATED AT THE ADSORPTION END OF THE PHAGE PARTICLE.
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EMBL; AE007045; AAK46139.:
PIR; C70720; C70720.
TIGR; MT1866; -.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hoiroyd S
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PE-PGRS family protein Rv1818c.
RV1818C OR MT1866 OR MTCY1A11.25C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria;
Corynebacterineae; Mycoba
NCBI_TaxID=1773;
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                                                                                                                                                                                 Pro; IPR000084; PE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 GGGSGGGSEG
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                                                                                                                                             protein;
                             AAK46139.1; ALT_INIT
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Best Local S
Matches 9
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K.,
Gordon S.V., Eiglmeier K.,
Gordon J., Molle S., Hamlin N., Holroyd S.,
Goliver S., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Goliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Goliver S., Seeger K., Skelton S., Squares S., Squares R.,
Goliver S., Seeger K., Skelton S., Squares S., Squares R.,
Goliver S., Seeger K., Whitehead S., Barrell B.G.;
The Complete genome sequence.";
U. Nature 393:537-544(1998).
C. --INTERNATIY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
            Query Match
Best Local
 Matches
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                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Et the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria;
Corynebacterineae; Mycobac
NCBI_TaxID=1773;
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                                                SEQUENCE
                                                                                                                                                                          EMBL; AL022022; CAA17745.1; -.
                                                                                      Hypothetical
SIGNAL
                                                                                                                                                    PIR; F70806; F70806. TubercuList; Rv3508;
                                                                                                                ProDom;
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8; Conserv
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281
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Conservative
                                                                                                  protein;
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64.3%;
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57.1%;
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family protein Rv3508 pr
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MISSING (IN REF. 2).
G -> GAGG (IN REF. 2).
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HYPOTHETICAL PE-PGRS
RV3508.
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    2;
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01-OCT-1996
01-OCT-1996
01-OCT-1996
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MEDLIND=91218803; PubMed=2090943;
Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;

"Sequence comparison of allelic forms of the Plasmodium famerozoite surface antigen MSA2.";

MOI. Biochem. Parasitol. 43:211-220(1990).

MOI. BIOCHEM. PARAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT
                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a class the European Bloinformatics and the EMBL the European Bloinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum (isolate 7G8
Eukaryota; Alveolata; Apicomplexa;
NCBI_TaxID=57266;
DJB1_HUMAN
P25685;
01-MAY-1992
01-OCT-1996
15-SEP-2003
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SEQUENCE
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                                                     HUMAN
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SUBCELLULAR LOCATION: Attached to the membrane
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9; Conserv
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(Rel.
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276 AA;
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 (Rel. 22, Created)
(Rel. 34, Last sequence update)
(Rel. 42, Last annotation updat
                                                                                                                                           Conservative
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64.3%;
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N-SFRA62A70400DEB2 CI
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(BY SIMILARITY).
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POLY-THR.
                                                                                                                                                                                                                                                                                             MEROZOITE
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exa; Haemosporida; Plasmodium
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(MSA-2)
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12;
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the Plasmodium falciparum
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RC TISSUE-Brain, and Lung;
RX MEDLINE-22388257; PubMed-12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wackernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Gener
                                                                          This SWISS-PROT entry is copyright. It is produced through a contween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                    STRUCTURE BY NMR OF 1-76.
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MEDLINE-97131529; PubMed-8975727;

Hata M., Okumura K., Seto M., Ohtsuka K.;

"Genomic cloning of a human heat shock protein 40 (Hsp40) gene (HSPF1)
and its chromosomal localization to 19p13.2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 197:235-240(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning of a cDNA for heat-shock protein hsp40, a bacterial DnaJ.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A human homologue of the Escherichia coli DnaJ heat-shock protein.";
Nucleic Acids Res. 19:6645-6645(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) (Heat shock protein 40) (HSP40) (DnaJ protein homolog 1) (HDJ-1).

DNAJB1 OR HSPF1 OR DNAJ1 OR HDJ1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohtsuka K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94071949; PubMed-8250930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human) Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92093635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                       send an
non-profit institutions as long as its content is and this statement is not removed. Usage by and for requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sc1. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-48.
                                                                     There are no rest
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                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                          human Hsp40
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                                                                                                                             a collaboration - MBL outstation -
                         .ch/announce/
                                                                               in
                                                                               0 On
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                                                                                                                                                                                                                                                                                                                                                                   RESULT
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EMBL;
EMBL;
EMBL;
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LORI_MOUSE
ID LORI_M
AC P18165
DT 01-NOV
DT 08-FEB
DE LORICE
GN LOR.
OS Mus mw
OC Eukary
OC Mammal
OX NCEL[]
RN [1]
RP SEQUE;
RX MEDLI!
RA Mehre.
                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                              LORI_MOUSE
P18165;
01-NOV-1990
01-NOV-1990
28-FEB-2003
    SEQUENCE FROM N.A. MEDLINE-90275605; Mehrel T., Hohl D.
                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                          TURN
HELIX
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SEQUENCE
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CONFLICT
CONFLICT
                                                                                                      Coricrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00625; DNAJPROTEIN SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heat shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00226; DnaJ; 1. Pfam; PF01556; DnaJ_C; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPRO02939; DnaJ_C.
InterPro; IPRO01623; DnaJ_N.
InterPro; IPRO03095; Hsp_DnaJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO: 0003773; F: heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; X62421; CAA44287.1; -...; D49547; BAAD8495.1; -...; D85429; BAA12819.1; -...; BC002352; AAH02352.1; BC019827; AAH19827.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JN0912; JN0912.
S20062; S20062.
                                                                                                                                                                                                                  74 GSGPSGGSGGGANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   604572;
                                                                                                                                                                                                                                      1 GDGSSGGSGGASTG
                                                                                                                                                                                                                                                             Similarity 64.3
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:5270; DNAJB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00636; DNAJ_1; 1.
PS50076; DNAJ_2; 1.
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33
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67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Chaperone; 170
1 70
11 11
13 28
                                                                                                              (Rel. 16, Created)
(Rel. 16, Last seq
(Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NOV-96
                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                           STANDARD;
              PubMed=2190691;
                                                                                                                                                                                                                                                                                                       1150
1183
320
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110
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   Rothnagel
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136
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64.3%;
tive
                                                                                                            Last sequence update)
Last annotation update)
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G -> L (IN REF. 1).

SGGGANGTSSEXTFHGDPHAMFAEFFGGRNPFDTFFFGQRNG
EEGMDIDDPFSGFPM -> TAREPMYPLSATHSMETLMPCL
LSSSVAEIPLTPFLGSGTGRKAWTLMTHSLASLW (IN
REF. 1).

R -> C (IN REF. 1).

M -> T (IN REF. 1).

V -> A (IN REF. 1).
                                                                                                                                                                                                                                                                      Score 50;
Pred. No.
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  J.A.,
                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L -> Q (IN REF. 1
RGASDEEIKRAYRRQA
                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein activity;
                                                                                                                                                                                                                                                                                                       17545098B0C196DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -DOMAIN
                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q (IN REF. 1).
  Longley M.A.,
                                                                                                                                                          481
                                                                                                                                                                                                                                                                      DB 1;
15;
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                                                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                                                                 Length 340;
                                                                                                                                                                                                                                                            Indels
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                                                      Euteleostomi;
Murinae; Mus
D.,
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RESULT 12
T711_HMAN
ID T711_H
Q9HCS4
AC Q9HCS4
AC 15-SEP
DT 15-SEP
DT 15-SEP
DT 15-SEP
DT 15-SEP
DT 15-SEP
CO TCF711
OS HOMO S
OC Eukary
OC Mammal
ON NCBI_T
RN [1]
RN [1]
RN [1]
RN SEQUEN
RY SEQUEN
RY "Miton
RT cancer
RT regula
RH Cancer
RT regula
RH [2]
RP SEQUEN
RM EDLII
RA MEDLII
RA CASTR
RT "A gen
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M34398; AAA39444.1; EMBL; U09189; AAA82152.1; PIR; A35628; A35628 A5628 A5628; BSSP; P02876; 9WGA. MGD; MGI:96816; Lor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T711_HUMAN SIGNARY
Q9HCS4; Q9NP00;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence upda
15-SEP-2003 (Rel. 42, Last annotation upda)
15-SEP-2003 (Rel. 47, Last annotation upda)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long as its content use by non-profit institutions as long as its content use as long as l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disepio D., Jones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keratinization.
"A gene family of HMG-box transcription 1.";
                                                                                                                                                                                                                                                                                   TISSUE=Fetal lung;
MEDLINE=20535962; Pul
Sagara N., Katoh M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                     SEQUENCE OF 331-419 FROM N.A. MEDLINE=92158676; PubMed=1741298;
                                                                                                                                                                                                                           cancer cell line MKN28
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCF7L1 OR TCF3
                                                                                                                                                                          Cancer
                                                                                                                                                                                                 regulation."
                                                                                                                                                                                                                                                         "Mitomycin
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLUTAMYL) LYSINE ISODIPEPTIDE BONDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGSSGGCGGGSGG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 AA;
                                                                                                                                                                                                                              C resistance induced by TCF-3 overexpression line MKN28 is associated with DT-diaphorase
                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa; Chordata; C
Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                     331-419
                                                                                                                                                                             60:5959-5962(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=7738016;
A., Longley M.A
                                                                                                                                                                                                                                                                                                                   PubMed=11085512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37830 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 м.а.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97349A786FF239FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription
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                                         factors with homology to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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RESULT 13
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EMBL; X62870;
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  YD25_MYCTU STA)
Q10637;
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01-OCT-1996 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Am. J. Pathol. 154:29-35(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005634; C:nucleus; NAS.
GO; GO:000700; F:transcription factor activity; NAS.
GO; GO:0006325; P:establishment and/or maintenance of chromat.
GO; GO:0006325; P:regulation of transcription, DNA-dependent; NAS
GO; GO:0030111; P:regulation of Wnt receptor signaling pathway; NI
InterPro; IPRO00910; HMG_12_box.
Pfam; PF00505; HMG_box; 1.
SMART; SM00398; HMG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barker N., Huls G., Korinek V., Clevers H.; "Restricted high level expression of Tcf-4 protein in intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99113953;
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DOMAIN
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COMPLEX (By simila
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FUNCTION: Participates in the Wnt signaling pathway. Binds to Dr. PUNCTION: Participates in the absence of CTNNB1, and as activated and acts as repressor in the absence of CTNNB1, and as activated in its presence. Necessary for the terminal differentiation of ints presence. Necessary for the terminal differentiation of the participation of the participation.
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                                                                                                                                                                                                                                                                                                         Conservative
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2LEF.
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                                                                                STANDARD;
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., Korinek V., Clevers H.;
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Pred. No.
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Mismatches
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole genome comparison of laboratory strains.";
Submitted (APR-2001) to the
-i- SIMILARITY: BELONGS TO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PE-PGRS family protein Rv1325c precursor.
RV1325C OR MT1367 OR MTCY130.10C.
                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                              Hypothetical
SIGNAL
                                                                                                                                                                                                                                                                      Pfam; PF00934; PE;
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TubercuList; Rv1325c;
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                                                                                                                                                                                                                                                                                                                                            EMBL; AE007010; AAK45630.1;
                                                                                                                                                                                                                                                                                                                                                         EMBL; 273902; CAA98089.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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8; Conserv
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                                                        Conservative
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TO THE MYCOBACTERIAL PE FAMILY. PGRS
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G -> D (I
G -> D (I
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                                                                     Score 50;
Pred. No.
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3; Mismatches
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RESULT 14

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AC Q9VVX3; Q94916;
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Best Local :
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-I- FUNCTION: INVOLVED IN THE DEVELOPMENT OF THE DROSOPHILA SYSTEM AND OCELLAR VISUAL STRUCTURES.

-I- SUBCELLULAR LOCATION: Nuclear (Probable).

-I- DEVELOPMENTAL STAGE: EXPRESSED IN THE ANTERIOR REGION OF EMBRYO BEFORE CELLULARIZATION AND BECOMES LOCALIZED TO TEMBRYO BEFORE CELLULARIZATION AND BECOMES LOCALIZED TO TEMBRYO BEFORE CELLULARIZATION GASTRULATION.

-I- DOMAIN: CONTAINS MULTIPLE REPEATS CONSISTING OF SINGLE ACTIVALULARIZATION.

-I- DOMAIN: CONTAINS MULTIPLE REPEATS CONSISTING OF AMINO ACIDS OF TAXABLE AND ASIN AND PAIRS OF AMINO ACIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Finkelstein R., Smouse D., Capaci T.M., Sprace
"The orthodenticle gene encodes a novel homeo
in the development of the Drosophila nervous
visual structures.";
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                      ProDom; PD000010; Homeobox; 1. SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X58983; CAA41732.1;
PIR; A35912; A35912.
HSSP; P06601; IFJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                              Transcription
DNA_BIND
                                                                                                                                                                                                                                                                                                        PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0004102; oc.
InterPro; IPR001356; Homeobox.
InterPro; IPR007104; Paired_homeo.
Pfam; PF00046; homeobox; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Enteropean Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
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9; Conserv
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RA Ballew R. M. Basu A. Baxendale J., Butres Figuration, Beast W. J., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Beeson K.Y. Benos P.V. Berman B.P., Bhandari D., Bolshakov S., Ra Beeson K.Y. Benos P.V., Berman B.P., Brokstein P., Brottier P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Ra Codson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Brottier C., Gabrielian A.E., Garg W.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Fosler C., Gabrielian A.E., Garg W.S., Gelbart W.M., Glasser K., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Ra Hostin D., Houston K.A., Howland T.J., Wei M., H., Ibegwam C., Levitsky A.A., Li J., Li Z., Kulp D., Lai Z., Kalsh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A. Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai Z., Kalsh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A. Nelson D.R., Welson K.A., Nixon K., Nusskern D.R., Pacieb J.M., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Palazzolo M., Pittman G.S., Fan S., Pollard J., Puri V., Reese M.G., Ra Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Ra Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Wang S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ra Kimmel B.E., Solden R., Engelot G., Zhong W., Zhou X., Smith H.O., The genome sequence of Drosophila melanogaster.", The genome sequence of Drosophila melanogaster.", Smith H.O., Let M., Weissen M., Strong R., Strong
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Bhanot P., Brink M.,
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Eukaryota; Metazoa; Arthropoda; Hexa
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"A new member of the frizzled family from Drosophila functions as
                                              FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with 6-proteins. Required to coordinate the cytoskeletons of epidermal cells to produce a parallel array of cuticular hairs and bristles.
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PubMed-8717036;
J. Samos C.H., Hsieh J.C., Wang Y., Macke J.P.,
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Muscomorpha;
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FlyBase; FBgn0016797; fz2.
G0; G0:0016021; C:integral t
G0; G0:0017147; F:Wnt-prote;
G0; G0:0007163; P:establish
G0; G0:0016055; P:Wnt recept
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CARBOHYD
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CONFLICT
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000539; Frizzled.
InterPro; IPR000024; Fz_domain
InterPro; IPR0000832; GPCR_secro
Pfam; PF01534; Frizzled; 1.
Pfam; PF01392; Fz; 1.
                        SEQUENCE
                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0489; FRIZZI SMART; SM00063; FRI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institu modified and this statement entities requires a license
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                                                                                                                                                 DOMAIN
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PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 frizzled (FZ) domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between 15 and 70 per cent of egg length, including the invaginating cells of the ventral furrow. Stripe pattern is emerging by early stage 8. From stage 9 and continuing throughout embryogenesis, expression is seen in the developing CNS. At stage 10, expressed in 15 stripes in the presumptive head and trunk regions, in the posterior midgut primordium, in a subset of cells of anterior midgut invagination and in the procephalic lobe. At stage 12, expression declines in epidermis and increases in the midgut and visceral mesoderm. At stage 17, only expressed in the CNS, hindgut and dorsal vessel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Wnt/beta-catenin signaling pathway (By similarity). DOMAIN: The fz domain is involved in binding with Wnt ligands.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U65589; AAC47273.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               family; Receptor;
                                                                  Lys-Thr-X-X-X-Trp motif is involved in the activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bioinformatics Institute. The profit institutions as long
                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                        C:integral to membrane; NAS.
F:Wnt-protein binding activity; IDA.
P:establishment and/or maintenance of cell
P:Wnt receptor signaling pathway; IDA.
                                                                                                                                                                                                                                                                                                                                                                           FRIZZLED.
                                             license agreement
                         75451 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           Fz_domain.
GPCR_secretin.
                                                                                                                                                                                                                                                                                                                    Wnt
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                                                                                                                                                                                                                                                                                                                  signaling pathway;
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                                                                                                                                                                                                                                                                                                                               G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is not removed.
  Score 50;
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                                                       N-LINKED (GLCNAC. .
                                                                   PDZ-BINDING.
N-LINKED (GI
                                                                                                                                                                                                                 3 (POTENTIAL)
CYTOPLASMIC (
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                                                                                                                GLY-RICH
                                                                                                                                                                                                       4 (POTENTIAL)
                                                                                       LYS-THR-X-X-X-TRP MOTIF.
                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                              FRIZZLED PROTEIN
                                    -> A (IN REF. 1)
-> T (IN REF. 1)
                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                        (POTENTIAL).
                         6C510F13CBAFB096 CRC64;
                                                                                                                                      (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                                                                                               receptor;
Length 694;
                                                        (POTENTIAL).
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Query Match

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			Search completed: August 20, 2003, 12:34:50 Job time : 7.42436 secs	Best Local Similarity 75.0%; Pred. No. 30; Matches 9; Conservative 2; Mismatches Oy 3 GSSGGSGGSGSGSTG 14
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Result
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Perfect score:
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050396 mycobacteri
08vj19 mycobacteri
091k43 arabidopsis
076546 dictyosteli
053552 mycobacteri
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092k72 rhizobium m
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09c2x0 cladosporiu
053804 mycobacteri
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091811 leishmania
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neurospora
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## ALIGNMENTS

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Matches 10
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01-OCT-2000 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
P0009G03.13 protein.
P0009G03.13.
                                                                                                                                                        STRAIN-CV. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0009603.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP00252; BAB03613.1;
Gramene; Q9LGJ3;
InterPro; IPR000834; Zn_carbOpept.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
SEQUENCE 537 AA; 58755 MW; F9069BABA60A271D CRC64;
                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9LGJ3
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                                                                                                            Similarity 71., 10; Conservative
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PS00133; CARBOXYPEPT_ZN_2; 1.

PS00133; CARBOXYPEPT_ZN_2; 1. CRC64;

: 537 AA; 58755 MW; F9069BABA60A271D CRC64;
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A COle S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

A Rutter S., Seeger K., Skelton S., Squares R.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares S.,

A Rutter S., Seeger K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

"Decipher 393:537-544(1998)."
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ŚTRAIN=CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Els

Peterson J., DeBoy R., Dodson R

Kolonay J.F., Nelson W.C., Umay;

Delcher A., Utterback T., Weidme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8VJ19 PRELIMINARY;
Q8VJ19;
01-MAR-2002 (TrEMBLrel 2
01-MAR-2002 (TrEMBLrel 2
01-MAR-2003 (TrEMBLrel 2
01-MAR-2003 (TrEMBLrel 2
PE_PGRS family protein.
MT3476.
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01-JUN-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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ProDom; PD001223; PE_region; 1.
PROSITE; PS00583; PFKB_KINASES_1; 1.
                                                                    laboratory strains.";
submitted (APR-2001) to the
EMBL; AE007154; AAK47814.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinobacteriaceae; Mycobacterium.

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       InterPro;
                                                                                                                                                                                                                  Bishai W.;
                                                                                                                                                                          Whole genome comparison of Mycobacterium tuberculosis clinical and
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                            Eisen J.A.,
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InterPro; IPR002173; PfkB.
Pfam; PF09934; PE; 1.
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01-OCT-2000 (TIEMBLIFE! 23, Last sequence update)
01-MAR-2003 (TIEMBLIFE! 23, Last annotation update)
51milarity to receptor protein kinase.
Arabidopsis thaliana (Mouse-ear cress).
Enkaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core elegermatophyta; Magnoliophyta; Bubassicatea; Arabidopsis.
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Prodom; PD001223; PE_region; 1.

PROSTTE; PS00588; PFKB_KINASES_1; 1.

SEQUENCE 628 AA; 53828 MW; 9F62B1E7CC2C567E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko T., Kato T., Submitted (JUL-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eurosids II; Brassicales; Brassicaceae; NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9LK43;
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                                                                                                                                                                                                                           pfam; pF00560; LRR; 9:
pfam; pF00059; pkinase; 1.
probom; pp000001; prot_kinase; 1.
prOSITE; pS50502; LRR_PS; 4.
pROSITE; pS00107; pROTEIN_KINASE_ATP; 1.
pROSITE; pS00108; pROTEIN_KINASE_ST; 1.
pROSITE; pS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                   Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structural analysis
                                                                                                                                                                                                         ATP-binding; Kinase; Receptor;
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11; Conserv
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GDGSSPGTGGASGG
                                         GDGSSGGSGGASTG
                                                                                                                                                                928 AA;
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                                                                                  Conservative
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                                                                                                                                                                    99964 MW;
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83.3%;
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the regions of
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78.6%;
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                                                                                  1;
                                                                                                        Score 55;
Pred. No.
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                                                                                                                                                                    13BB63639060B412 CRC64;
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ACCIE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
AGORDON S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
AA Gordon S.V., Eiglmeier K., Gas S., Chillingworth T., Connor R.,
AA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
AA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
AA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
AA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
AA Rutter S., Seeger K., Skelton S., Squares R.,
AR Rutter S., Seeger K., Skelton S., Squares R.,
AR Rutter S., Seeger K., Skelton S., Squares R.,
AR Rutter S., Seeger K., Whitehead S., Barrell B.G.;
AP Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
AR LAC22022; CAA17744.1; -.
BR InterPro, IPR002952; Eggshell.
BR InterPro; IPR002173; pfkB.
BR InterPro; IPR002173; pfkB.
BR InterPro; IPR002173; pfkB.
                                                                        Query Match
Best Local
                                                        Matches
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Best Local
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DG1105.
Dictyostelium discoideum (Slime mold).
Dictyostelium discoideum (Slime mold).
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01-NOV-1998
01-OCT-2002
                                                                                                                                                 PRINTS; PR01228; EGGSHELL.
PROSITE; PS00583; PFKB_KINASES_1;
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RV3507 OR MTV023.14.
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; A
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01-JUN-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Submitted (JUL-1998) to the
EMBL; AF076601; AAC31540.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterineae;
NCBI_TaxID=1773;
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11; Conserv
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1381 AA;
     GDGSSGGSGGASTG
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vA; 112463
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                                                                   75.3%;
64.3%;
                                                                                                                     110624 MW;
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08,
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                                                Score 55; DB Pred. No. 55; 3; Mismatches
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Last sequence update)
Last annotation update)
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                                                                                                                 CA09676BD07F6482 CRC64;
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RX KEDLINE-9825987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I.

RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., Rajandream M.A., Rogers J.,

RA Hornsby T., Sebetton S., Squares R.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

Bulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:337-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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01-MAR-2002 (TrEMBLrel. 20, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno-
PGRS-family (PE_PGRS family protein)
RV2490C OR MT2564 OR MTV008.46C.
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White Celeischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzbe Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Miku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.".

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AE007163; AAK47970.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8VIZ1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacte
Corynebacterineae; Mycobacteriaceae;
CORJ_TaxID=1773;
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01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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A; 110839 MW;
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Last sequence update)
Last annotation updat
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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124AC8AAADD55EBD CRC64;
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                                                                                                                                                                     Holroyd
                                                                                                                                                                                                                                     Harris D.,
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POST PRESENTATION OF THE P
RESULT 10
Q8LK71
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Q92K72;
Q92K72;
Q92K72;
Q92K72;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-1003 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2004 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 20, Last sequence update)
Q1-
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ EMBL; ALO21246; CAA16067.1; ALT_INIT. EMBL; AE007093; AAK46868.1; -
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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Baft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.

Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; MT2564; -. TubercuList; Rv2490c; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.", Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proDom; pD001223; PE_region; 1.
proSITE; pS00583; PFKB_KINASES_1; 1.
proSITE; pS01287; RTC; 1.
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InterPro; IPR002173; PfkB.
InterPro; IPR000228; RNA3'_term_cycl
                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete
SEQUENCE
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9; Conserv
                                                                                                                                                                                                                                                                                                                                     Similarity.
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57 AA;
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                                                                                                                                                   GSGSMGGSGGGSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                               5230 MW;
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64.3%;
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71.4%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                 Score 54; DB pred. No. 2.8;
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                                                                                                                                                                                                                                                                                                   Mismatches
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ACCOMPANDA SOLUTION OF SOLUTIO
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Q9C2X0
                                                        RESULT 12
053844
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Q8LK71;
Q1-OCT-2002
01-OCT-2002
01-MAR-2003
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01-JUN-2001
01-OCT-2002
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smART; SM00499; AAI; 1.
seQUENCE 179 AA; 17117 MW; 7
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                                                                                                                                                                                                                                                                                                                                      Nielsen P.S., Clark A.J., Oliver R.B., Huber M., Spanu *HCf-6, a novel class II hydrophobin from Cladosporium Microbiol. Res. 156:1-5(2001).
EMBL; AJZ51294; CAC27407.1; -.
InterPro; IPR002952; Eggshell.
PRINTS; PR01228; EGGSHELL.
CHAIN 17 184 HYDROPHOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-cv. maple ar Farah S., Singh J.;
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SEQUENCE
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STRAIN=21265535; PubMed=11372645;
MEDLINE=21265535; PubMed=11372645;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Dothideomycetes et Chaetothyriomycetes incertae sedis;
Mycosphaerellaceae; mitosporic Mycosphaerellaceae; Cla
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HCF-6.
053844;
01-JUN-1998
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82 GSGGSGGSGGSST 94
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                                                                                                                                                                                                                                                                                                                  184 AA;
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17147 MW;
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Last sequence update)
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EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                 Score 54; DB pred. No. 9.4; 3; Mismatches
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                                                                                                                                                                                                                                                                             Length 184;
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| fulvum.";
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Best Local s
Matches s
SEQUENCE FROM N.A.

STRAIN-H37RV;
MEDLINE-98295987; PubMed-9634230;
COLE S.T., Brosch R., Parkhill J., Garnier T., Chur.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III., '
Badcock K., Basham D., Brown D., Chillingworth T., '
Badcock R., Devlin K., Feltwell T., Gentles S., Haml
                                                                                                                                                                                                           O53809 PRELIMINARY; PRT; 783 AA.
O53809;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
PGRS-family protein (PE_PGRS family protein).
RV0746 OR MT0772.1 OR MTV041.20.
MYCOBacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacterium.
COrynebacterineae; Mycobacteriaceae; Mycobacterium.
CORJENSE: Nycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.";
Submitted (APR-2001) to the
EMBL; AL022004; CAA17639.1;
EMBL; AE006974; AAK45096.1;
TIGR; MT0854.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., H Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hollornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy Oliver S., Ogborne J., Quail M.A., Rajandream M.A., Rogers J. Rutter S., Seeger K., Skelton S., Squares S., Squares T., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from tomplete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen

Feterson J., DeBoy R., Dodson R.,

Kolonay J.F., Nelson W.C., Umayam

Delcher A., Utterback T., Weidman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
PGRS-family protein (PE_PGRS family protein).
RV0833 OR MT0854.1 OR MTV043.25.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TubercuList; Rv0833; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole genome comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterineae;
NCBI_TaxID-1773;
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Cole S.T., Brosch
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9; Conser
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69.28;
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Pred. No.
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-> G (IN REF. 2).
C3C91307F9A8A2EC
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ed. No. 40;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Length 749;
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                                                                           Churcher C.,
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                               Tekaia
Connor
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       Holroyd
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RESULT
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Synechocystis sp. strain PCC6803. II. Sentire genome and assignment of potenti DNA Res. 3:109-136(1996).

EMBL; D90907; BAA17634-1; ...
Interpro; IPR003644; Calx_beta.
Interpro; IPR002860; GH_BNR.
Interpro; IPR001343; Hemlysn_Ca_bind.
Interpro; IPR000413; Integrin_alpha.
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Best Local
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01-FEB-1997 (
01-FEB-1997 (
01-OCT-2002 (
Hypothetical
SLR1403
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Submitted (APR-2001) to the E EMBL; AL021958; CAA17513.1;
EMBL; AE006968; AAK45009.1;
TIGR; MT0772.1;
                                                                                                                                                                                                                                              Kaneko T., Sato S., Kotani H., Tar
Miyajima N., Hirosawa M., Sugiura
Hosouchi T., Matsuno A., Muraki A.
Shimpo S., Takeuchi C., Wada T., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechocystis sp. (strain Bacteria; Cyanobacteria; 
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-97061201; PubMed-8905231;
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                                                                                                                                                                                                                Sequence analysis
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InterPro; IPR000817;
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Kolonay J.F., Nelson W.C., Umayam
Delcher A., Utterback T., Weidman
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Fleischmann R.D., Alland D., Eisen
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783 AA;
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7 (TrEMBLrel. 02, L
2 (TrEMBLrel. 22, L
al protein slr1403.
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76.9%;
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Quail M.A., Rajandream M.A.,
Skelton S., Squares S., Squares
Whitehead S., Barrell B.G.,
Whitehead S., Barrell B.G.,
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, Sugiura M., Sasamoto S.
Muraki A., Nakazaki N.,
Wada T., Watanabe A., Yan
                                                                                                                                                                                       PCC6803. II. S.
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Last annotation updat
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    II. Sequence determination of
potential protein-coding regions

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, Gwinn M., H
n L.A., Ermol
n J., Khouri
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, Ermolaeva M., S
Khouri H., Gill J
                                                                                                                                                                                                                                        Asamizu L.
TOTO S., Kimu.
Naruo K.,
Aa M., Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hickey E.,
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Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                Query Match 72.6%; Score 53; DB 5; Length 362; Best Local Similarity 71.4%; Pred. No. 25; Matches 10; Conservative 1; Mismatches 3; Indels
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pfam; pF03160; Calx-beta; 1.

pfam; pF01839; FG-GAP; 8.

pfam; pF00353; hemolysinCabind; 6.

pRINTS; pR00313; CABNDNGRPT.

PRINTS; PR01185; INTEGRINA.

SMART; SM00237; Calx_beta; 1.

SMART; SM00191; Int_alpha; 11.

Hypothetical protein; Complete proteome.

SEQUENCE 3016 AA; 311507 MW; B34D83B005D0717A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 37.3 kDa protein.
L3238.09
                                                                                                                                                                                                                                                                                                                                                                                                "A physical map of the Leishmania major Friedlin genome."; Genome Res. 8:135-145(1998).

EMBL; AL133468; CAB63136.1; -.

Hypothetical protein.

SEQUENCE 362 AA; 37271 MW; 4FB3EC8976A956C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-Friedlin;
MEDLINE-98146435; PubMed-9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRALN=Friedlin;
Wedler H., Hilbert H., Duesterhoeft A., Ivens A.C., Murphy L.,
Wedler H., Rajandream M.A., Barrell B.G.;
Quall M., Rajandream M.A., Barrell B.G.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leishmania major.
Eukaryota; Euglenozoa;
MCBI_TaxID=5664;
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                                                                                                                                   301 GAGSSGGGGAAVG 314
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71.4%;
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